GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS COLON CANCER CELLS AND THEIR METHODS OF USE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of application serial no. 09/872,850, filed June 1, 2001, which application claims the benefit of U.S. Provisional Application Serial No. 60/208,871, filed June 2, 2000, which applications are incorporated by reference herein in their entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to polynucleotides of human origin and the encoded gene products that are differentially expressed in colon cancer cells.

BACKGROUND OF THE INVENTION

[0003] Cancer, like many diseases, is not the results of a single, well-defined cause, but rather can be viewed as several diseases, each caused by different aberrations in informational pathways, that ultimately result in apparently similar pathologic phenotypes. Identification of polynucleotides that correspond to genes that are differentially expressed in cancerous, pre-cancerous, or low metastatic potential cells relative to normal cells of the same tissue type, provides the basis for diagnostic tools, facilitates drug discovery by providing for targets for candidate agents, and further serves to identify therapeutic targets for cancer therapies that are more tailored for the type of cancer to be treated. Identification of differentially expressed gene products also furthers the understanding of the progression and nature of complex diseases such as cancer, and is key to identifying the genetic factors that are responsible for the phenotypes associated with development of, for example, the metastatic phenotype. Identification of gene products that are differentially expressed at various stages, and in various types of cancers, can both provide for early diagnostic tests, and further serve as therapeutic targets and the basis for screening assays to identify chemotherapeutic agents that modulate the activity (*e.g.*, expression, biological activity, and the like) of the gene product of the differentially expressed gene.

[0004] Early disease diagnosis, especially in diseases such as cancer, is of central importance to halting disease progression, and reducing morbidity. Analysis of a patient's tumor to identify the gene products that are differentially expressed, and administration of therapeutic agent(s) designed to modulate the activity of those differentially expressed gene products, provides the basis for more specific, rationale cancer therapy, which therapy may result in diminished adverse side effects relative to conventional therapies. Furthermore, confirmation that a tumor poses less risk to the patient (*e.g.*, that the tumor is benign) can avoid unnecessary therapies. In short, identification of genes and the encoded gene products that are differentially expressed in cancerous cells can provide the basis of therapeutics, diagnostics, prognostics, therametrics, and the like.

[0005] In exemplary aspects, the invention described herein provides colon cancer diagnostics, prognostics, therametrics, and therapeutics based upon polynucleotides and/or their encoded gene products.

SUMMARY OF THE INVENTION

[0006] The present invention provides methods and compositions useful in detection of cancerous cells, identification of agents that modulate the phenotype of cancerous cells, and identification of therapeutic targets for chemotherapy of cancerous cells. Cancerous colon cells are of particular interest in each of these aspects of the invention. More specifically, the invention provides polynucleotides, as well as polypeptides encoded thereby, that are differentially expressed in cancerous colon cells relative to normal colon cells. These polynucleotides and polypeptides are thus useful in a variety of diagnostic, therapeutic, and drug discovery methods. In some embodiments, a polynucleotide that is differentially expressed in colon cancer cells can be used in diagnostic assays to detect colon cancer cells. In other embodiments, a polynucleotide that is differentially expressed in colon cancer cells, and/or a polypeptide encoded thereby, is itself a target for therapeutic intervention.

[0007] Accordingly, in one aspect the invention features a method of diagnosing colon cancer in a subject, the method comprising detecting a level of expression of a gene product in a test colon cell sample obtained from a subject, wherein the gene product is

encoded by a gene identified by a polynucleotide corresponding to a gene differentially expressed in cancerous colon cells; and comparing the level of expression of the gene product in the test sample to a level of expression of the gene product in a normal colon cell; wherein detection of an expression level in the test sample that is significantly different from the level of expression in a normal cell indicates that the test cell is cancerous.

[0008] In another aspect, the invention features a method for assessing the cancerous phenotype (*e.g.*, metastatis, aberrant cellular proliferation, and the like) of a colon cell comprising: detecting a level of expression of a gene product in a test colon cell sample, wherein the gene product is encoded by a gene differentially expressed in a cancerous colon cell; and comparing a level of expression of the gene product in the test colon cell sample with a level of expression of the gene product in a control cell sample; wherein the level of expression of the gene product in the test cell sample relative to the level of expression in the control cell sample is indicative of the metastatic potential of the test cell sample.

[0009] In another aspect the invention features a method for inhibiting growth of a cancerous colon cell comprising introducing into a cancerous mammalian cell an antisense polynucleotide for inhibition of expression of a gene differentially expressed in a cancerous colon cell, wherein inhibition of expression of the gene inhibits growth of the cancerous cell.

[0010] In another aspect, the invention features a method for assessing the tumor burden of a subject, the method comprising: detecting a level of a gene product in a test sample from a subject, the test sample suspected of comprising a gene product encoded by a gene differentially expressed in a cancerous colon cell, the gene product being encoded by a gene differentially expressed in a cancerous colon cell; wherein detection of the level of the gene product in the test sample is indicative of the tumor burden in the subject.

[0011] In another aspect, the invention features methods for identifying agents that have activity in modulating (*e.g.*, decreasing) a biological activity of a differentially expressed gene product.

[0012] In another aspect, the invention features methods for identifying a gene product as a therapeutic target for treatment of colon cancer.

[0013] These and other objects, advantages, and features of the invention will become apparent to those persons skilled in the art upon reading the details of the invention as more fully described below.

BRIEF DESCRIPTION OF THE DRAWING

[0014] Fig. 1 is a schematic showing the alignment of the sequences (represented by single lines) that resulted in the assembly of the contig (represented by the bars in the lower portion of the figure).

DETAILED DESCRIPTION OF THE INVENTION

[0015] Before the present invention is described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[0016] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications and patent applications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

[0017] It must be noted that as used herein and in the appended claims, the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the colon cancer cell" includes reference to one or more cells and equivalents thereof known to those skilled in the art, and so forth.

[0018] The publications and applications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may

be different from the actual publication dates which may need to be independently confirmed.

Definitions

[0019] The terms "polynucleotide" and "nucleic acid", used interchangeably herein, refer to a polymeric forms of nucleotides of any length, either ribonucleotides or deoxynucleotides. Thus, these terms include, but are not limited to, single-, double-, or multi-stranded DNA or RNA, genomic DNA, cDNA, DNA-RNA hybrids, or a polymer comprising purine and pyrimidine bases or other natural, chemically or biochemically modified, non-natural, or derivatized nucleotide bases. These terms further include, but are not limited to, mRNA or cDNA that comprise intronic sequences (see, *e.g.*, Niwa et al. (1999) Cell 99(7):691-702). The backbone of the polynucleotide can comprise sugars and phosphate groups (as may typically be found in RNA or DNA), or modified or substituted sugar or phosphate groups. Alternatively, the backbone of the polynucleotide can comprise a polymer of synthetic subunits such as phosphoramidites and thus can be an oligodeoxynucleoside phosphoramidate or a mixed phosphoramidate-phosphodiester oligomer. Peyrottes et al. (1996) Nucl. Acids Res. 24:1841-1848; Chaturvedi et al. (1996) Nucl. Acids Res. 24:2318-2323. A polynuclotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, uracyl, other sugars, and linking groups such as fluororibose and thioate, and nucleotide branches. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications included in this definition are caps, substitution of one or more of the naturally occurring nucleotides with an analog, and introduction of means for attaching the polynucleotide to proteins, metal ions, labeling components, other polynucleotides, or a solid support.

[0020] The terms "polypeptide" and "protein", used interchangebly herein, refer to a polymeric form of amino acids of any length, which can include coded and non-coded amino acids, chemically or biochemically modified or derivatized amino acids, and polypeptides having modified peptide backbones. The term includes fusion proteins, including, but not limited to, fusion proteins with a heterologous amino acid sequence,

fusions with heterologous and homologous leader sequences, with or without N-terminal methionine residues; immunologically tagged proteins; and the like.

[0021] "Heterologous" means that the materials are derived from different sources (*e.g.*, from different genes, different species, etc.).

[0022] As used herein, the terms "a gene that is differentially expressed in a colon cancer cell," and "a polynucleotide that is differentially expressed in a colon cancer cell are used interchangeably herein, and generally refer to a polynucleotide that represents or corresponds to a gene that is differentially expressed in a cancerous colon cell when compared with a cell of the same cell type that is not cancerous, e.g., mRNA is found at levels at least about 25%, at least about 50% to about 75%, at least about 90%, at least about 1.5-fold, at least about 2-fold, at least about 5-fold, at least about 10-fold, or at least about 50-fold or more, different (*e.g.*,, higher or lower). The comparison can be made in tissue, for example, if one is using in situ hybridization or another assay method that allows some degree of discrimination among cell types in the tissue. The comparison may also or alternatively be made between cells removed from their tissue source.

[0023] "Differentially expressed polynucleotide" as used herein refers to a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product; a non-coding sequence) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

[0024] "Corresponds to" or "represents" when used in the context of, for example, a polynucleotide or sequence that "corresponds to" or "represents" a gene means that a sequence of the polynucleotide is present in the gene or in the nucleic acid gene product (*e.g.*, mRNA). The polynucleotide may be wholly present within an exon of a genomic sequence of the gene, or different portions of the sequence of the polynucleotide may be present in different exons (*e.g.*, such that the contiguous polynucleotide sequence is

present in an mRNA, either pre- or post-splicing, that is an expression product of the gene). In some embodiments, the polynucleotide may represent or correspond to a gene that is modified in a cancerous cell relative to a normal cell. For example, the gene in the cancerous cell may be modified by insertion of an endogenous retrovirus, a transposable element, or other naturally occurring or non-naturally occurring nucleic acid. In such cases, the polynucleotide may include sequences of both the native gene (*e.g.*, the gene without the heterologous sequence) and the inserted, non-native sequence.

[0025] "Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy), and use of therametrics (*e.g.*, monitoring a subject's condition to provide information as to the effect or efficacy of therapy).

[0026] As used herein, the term "a polypeptide associated with colon cancer" refers to a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell.

[0027] The term "biological sample" encompasses a variety of sample types obtained from an organism and can be used in a diagnostic or monitoring assay. The term encompasses blood and other liquid samples of biological origin, solid tissue samples, such as a biopsy specimen or tissue cultures or cells derived therefrom and the progeny thereof. The term encompasses samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components. The term encompasses a clinical sample, and also includes cells in cell culture, cell supernatants, cell lysates, serum, plasma, biological fluids, and tissue samples.

[0028] The terms "treatment", "treating", "treat" and the like are used herein to generally refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete stabilization or cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes: (a)

preventing the disease or symptom from occurring in a subject which may be predisposed to the disease or symptom but has not yet been diagnosed as having it; (b) inhibiting the disease symptom, i.e., arresting its development; or relieving the disease symptom, i.e., causing regression of the disease or symptom.

[0029] The terms "individual," "subject," "host," and "patient," used interchangeably herein and refer to any mammalian subject for whom diagnosis, treatment, or therapy is desired, particularly humans. Other subjects may include cattle, dogs, cats, guinea pigs, rabbits, rats, mice, horses, and so on.

[0030] As used herein the term "isolated" refers to a polynucleotide, a polypeptide, an antibody, or a host cell that is in an environment different from that in which the polynucleotide, the polypeptide, the antibody, or the host cell naturally occurs. A polynucleotide, a polypeptide, an antibody, or a host cell which is isolated is generally substantially purified. As used herein, the term "substantially purified" refers to a compound (e.g., either a polynucleotide or a polypeptide or an antibody) that is removed from its natural environment and is at least 60% free, preferably 75% free, and most preferably 90% free from other components with which it is naturally associated. Thus, for example, a composition containing A is "substantially free of" B when at least 85% by weight of the total A+B in the composition is A. Preferably, A comprises at least about 90% by weight of the total of A+B in the composition, more preferably at least about 95% or even 99% by weight.

[0031] A "host cell", as used herein, refers to a microorganism or a eukaryotic cell or cell line cultured as a unicellular entity which can be, or has been, used as a recipient for a recombinant vector or other transfer polynucleotides, and include the progeny of the original cell which has been transfected. It is understood that the progeny of a single cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to natural, accidental, or deliberate mutation.

[0032] The terms "cancer", "neoplasm", "tumor", and "carcinoma", are used interchangeably herein to refer to cells which exhibit relatively autonomous growth, so that they exhibit an aberrant growth phenotype characterized by a significant loss of control of cell proliferation. In general, cells of interest for detection or treatment in the

present application include precancerous (*e.g.*, benign), malignant, pre-metastatic, metastatic, and non-metastatic cells. Detection of cancerous cell is of particular interest.

[0033] "Cancerous phenotype" generally refers to any of a variety of biological phenomena that are characteristic of a cancerous cell, which phenomena can vary with the type of cancer. The cancerous phenotype is generally identified by abnormalities in, for example, cell growth or proliferation (*e.g.*, uncontrolled growth or proliferation), regulation of the cell cycle, cell mobility, or cell-cell interaction.

[0034] "Therapeutic target" generally refers to a gene or gene product that, upon modulation of its activity (*e.g.*, by modulation of expression, biological activity, and the like), can provide for modulation of the cancerous phenotype.

[0035] As used throughout "modulation" is meant to refer to an increase or a decrease in the indicated phenomenon (*e.g.*, modulation of a biological activity refers to an increase in a biological activity or a decrease in a biological activity).

POLYNUCLEOTIDE COMPOSITIONS

[0036] The present invention provides isolated polynucleotides that represent genes that are differentially expressed in colon cancer cells. The polynucleotides, as well as polypeptides encoded thereby, find use in a variety of therapeutic and diagnostic methods.

[0037] The scope of the invention with respect to polynucleotide compositions useful in the methods described herein includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of the polynucleotide sequences provided herein; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; cDNAs corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions

contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicted.

[0038] The invention features polynucleotides that represent genes that are expressed in human tissue, specifically human colon tissue, particularly polynucleotides that are differentially expressed in colon cancer cells. Nucleic acid compositions described herein of particular interest comprise a sequence set forth in any one of the polynucleotide sequences provided herein or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, its complements and degenerate variants thereof, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of the polynucleotide sequences provided herein.

[0039] The polynucleotides useful in the methods described herein also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous

genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

[0040] In one embodiment, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of the polynucleotide sequences provided herein. That is, when at least 15 contiguous nt of one of the disclosed polynucleotide sequences is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one polynucleotide sequences provided herein can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, e.g., probes of a size within the range of about 18 nt , 25 nt, 50 nt, 75 nt or 100 nt, but in general about 15 nt represents sufficient sequence for unique identification.

[0041] Polynucleotides contemplated by the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants (*e.g.*, sequences that encode the same polypeptides but, due to the degenerate nature of the genetic code, different in nucleotide sequence), allelic variants, *etc.*). Variants of the polynucleotides contemplated by the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides described herein can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

[0042] The invention also encompasses homologs corresponding to any one of the polynucleotide sequences provided herein, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding

region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402.

[0043] In general, variants of the polynucleotides described herein have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

[0044] The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide. mRNA species can also exist with both exons and introns, where the introns may be removed by alternative splicing. Furthermore it should be noted that different species of mRNAs encoded by the same genomic sequence can exist at varying levels in a cell, and detection of these various levels of mRNA species can be indicative of differential expression of the encoded gene product in the cell.

[0045] A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the

introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

[0046] The nucleic acid compositions of the subject invention can encode all or a part of the naturally-occurring polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments contemplated by the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide provided herein. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from any one of the polynucleotide sequences provided herein.

[0047] Probes specific to the polynucleotides described herein can be generated using the polynucleotide sequences disclosed herein. The probes are preferably at least about a 12 nt, 15 nt, 16 nt, 18 nt, 20 nt, 22 nt, 24 nt, or 25 nt fragment of a corresponding contiguous sequence any one of the polynucleotide sequences provided herein, and can be less than 2 kb, 1 kb, 0.5 kb, 0.1 kb, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of any one of the polynucleotide sequences provided herein. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked

following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

[0048] The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

[0049] The polynucleotides described herein can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

[0050] The nucleic acid compositions described herein can be used to, for example, produce polypeptides, as probes for the detection of mRNA in biological samples (*e.g.*, extracts of human cells) or cDNA produced from such samples, to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of any one of the polynucleotide provided herein or variants thereof in a sample. These and other uses are described in more detail below.

POLYPEPTIDES AND VARIANTS THEREOF

[0051] The present invention further provides polypeptides encoded by polynucleotides that represent genes that are differentially expressed in colon cancer cells. Such polypeptides are referred to herein as "polypeptides associated with colon cancer." The polypeptides can be used to generate antibodies specific for a polypeptide associated with colon cancer, which antibodies are in turn useful in diagnostic methods, prognostics methods, therametric methods, and the like as discussed in more detail herein. Polypeptides are also useful as targets for therapeutic intervention, as discussed in more detail herein.

[0052] The polypeptides contemplated by the invention include those encoded by the disclosed polynucleotides and the genes to which these polynucleotides correspond, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of the polynucleotide sequences provided herein, or a variant thereof.

[0053] In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide described herein, as measured by BLAST 2.0 using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

[0054] The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal

or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST 2.0 algorithm, with the parameters described *supra*.

[0055] In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

[0056] Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted.

[0057] Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, e.g., Go *et al*, *Int. J. Peptide Protein Res.* (1980) *15*:211), the thermostability of the variant polypeptide (see, e.g., Querol *et al.*, *Prot. Eng.* (1996) *9*:265), desired glycosylation sites (see, e.g., Olsen and Thomsen, *J. Gen. Microbiol.* (1991) *137*:579), desired disulfide bridges (see, e.g., Clarke *et al.*, *Biochemistry* (1993) *32*:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) *7*:1379),

desired metal binding sites (see, e.g., Toma *et al.*, *Biochemistry* (1991) *30*:97, and Haezerbrouck *et al.*, *Protein Eng.* (1993) *6*:643), and desired substitutions with in proline loops (see, e.g., Masul *et al.*, *Appl. Env. Microbiol.* (1994) *60*:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314.

[0058] Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any one of the polynucleotide sequences provided herein, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

ANTIBODIES

[0059] The present invention further provides antibodies, which may be isolated antibodies, that are specific for a polypeptide encoded by a polynucleotide described herein and/or a polypeptide of a gene that corresponds to a polynucleotide described herein. Antibodies can be provided in a composition comprising the antibody and a buffer and/or a pharmaceutically acceptable excipient. Antibodies specific for a polypeptide associated with colon cancer are useful in a variety of diagnostic and therapeutic methods, as discussed in detail herein.

[0060] Gene products, including polypeptides, mRNA (particularly mRNAs having distinct secondary and/or tertiary structures), cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide,

and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

[0061] Methods for production of antibodies that specifically bind a selected antigen are well known in the art. Immunogens for raising antibodies can be prepared by mixing an antigen (*e.g.*, polypeptide) with an adjuvant, and/or by making fusion proteins with larger immunogenic proteins. Antigens (*e.g.*, polypeptides) can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Monoclonal antibodies can be generated by isolating spleen cells and fusing myeloma cells to form hybridomas. Alternatively, a polynucleotide encoding an antigen of interest is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein antigen generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

[0062] Preparations of polyclonal and monoclonal antibodies specific for an antigen (*e.g.*, polypeptide) are made using standard methods known in the art. For example, the antibodies can be produced so as ot specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, e.g., at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. In one embodiment, antibodies that specifically bind polypeptides contemplated by the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

[0063] The invention also contemplates naturally occurring antibodies. For example, serum antibodies to a polypeptide of interest in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the

corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

[0064] In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies (*e.g.*, chimeric antibodies, humanized antibodies, human antibodies produced by a transgenic animal (*e.g.*, a transgenic mouse such as the Xenomous™), antibody derivatives (e.g., single chain antibodies, antibody fragments (e.g., Fab, etc.)), according to methods well known in the art.

COMPUTER-RELATED EMBODIMENTS

[0065] In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. For example, in the instant case, the sequences of polynucleotides and polypeptides corresponding to genes differentially expressed in cancer, particular in colon cancer, as well as the nucleic acid and amino acid sequences of the genes themselves, can be provided in electronic form in a computer database.

[0066] In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a cancerous colon cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) colon cell.

[0067] The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the

representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

[0068] The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of sequence described herein. By plurality is meant at least 2, usually at least 3 and can include up to all of the sequences described herein. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

[0069] Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of the sequences described herein, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

[0070] One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of libraries comprising one or more sequence described herein can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc*, including, but not limited to, for example, search program software, *etc.*).

[0071] By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the gapped BLAST (Altschul *et al. Nucleic Acids Res.* (1997) *25*:3389-3402) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

[0072] As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

[0073] "Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information.

Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt A variety of comparing means can be used to accomplish comparison of sequence information from a sample (e.g., to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

[0074] A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but arc not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

[0075] A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile. A gene expression profile can be generated from, for example, a cDNA library prepared from mRNA isolated from a test cell suspected of being cancerous or pre-cancerous, comparing the sequences or partial sequences of the clones against the sequences in an electronic database, where the sequences of the electronic database represent genes differentially expressed in a cancerous cell, *e.g.,* a cancerous colon cell. The number of clones having a sequence that

has substantial similarity to a sequence that represents a gene differentially expressed in a cancerous cell is then determined, and the number of clones corresponding to each of such genes is determined. An increased number of clones that correspond to differentially expressed gene is present in the cDNA library of the test cell (relative to, for example, the number of clones expected in a cDNA of a normal cell) indicates that the test cell is cancerous.

[0076] As discussed above, the "library" as used herein also encompasses biochemical libraries of the polynucleotides of the sequences described herein, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of the genes described herein is represented by a sequence on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

[0077] In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by a gene corresponding to a sequence described herein.

DIAGNOSTIC AND OTHER METHODS INVOLVING DETECTION OF DIFFERENTIALLY EXPRESSED GENES

[0078] The present invention provides methods of using the polynucleotides described herein. In specific non-limiting embodiments, the methods are useful for detecting colon cancer cells, facilitating diagnosis of cancer and the severity of a cancer (*e.g.*, tumor grade, tumor burden, and the like) in a subject, facilitating a determination of the

prognosis of a subject, and assessing the responsiveness of the subject to therapy (*e.g.*, by providing a measure of therapeutic effect through, for example, assessing tumor burden during or following a chemotherapeutic regimen). Detection can be based on detection of a polynucleotide that is differentially expressed in a colon cancer cell, and/or detection of a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell ("a polypeptide associated with colon cancer"). The detection methods of the invention can be conducted *in vitro* or *in vivo*, on isolated cells, or in whole tissues or a bodily fluid, *e.g.*, blood, plasma, serum, urine, and the like).

[0079] In general, methods of the invention involving detection of a gene product (*e.g.*, mRNA, cDNA generated from such mRNA, and polypeptides) involves contacting a sample with a probe specific for the gene product of interest. "Probe" as used herein in such methods is meant to refer to a molecule that specifically binds a gene product of interest (*e.g.*, the probe binds to the target gene product with a specificity sufficient to distinguish binding to target over non-specific binding to non-target (background) molecules). "Probes" include, but are not necessarily limited to, nucleic acid probes (*e.g.*, DNA, RNA, modified nucleic acid, and the like), antibodies (*e.g.*, antibodies, antibody fragments that retain binding to a target epitope, single chain antibodies, and the like), or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target gene product of interest.

[0080] The probe and sample suspected of having the gene product of interest are contacted under conditions suitable for binding of the probe to the gene product. For example, contacting is generally for a time sufficient to allow binding of the probe to the gene product (*e.g.*, from several minutes to a few hours), and at a temperature and conditions of osmolarity and the like that provide for binding of the probe to the gene product at a level that is sufficiently distinguishable from background binding of the probe (*e.g.*, under conditions that minimize non-specific binding). Suitable conditions for probe-target gene product binding can be readily determined using controls and other techniques available and known to one of ordinary skill in the art.

[0081] In this embodiment, the probe can be a an antibody or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target polypeptide of interest.

[0082] The detection methods can be provided as part of a kit. Thus, the invention further provides kits for detecting the presence and/or a level of a polynucleotide that is differentially expressed in a colon cancer cell (*e.g.*, by detection of an mRNA encoded by the differentially expressed gene of interest), and/or a polypeptide encoded thereby, in a biological sample. Procedures using these kits can be performed by clinical laboratories, experimental laboratories, medical practitioners, or private individuals. The kits of the invention for detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell comprise a moiety that specifically binds the polypeptide, which may be a specific antibody. The kits of the invention for detecting a polynucleotide that is differentially expressed in a colon cancer cell comprise a moiety that specifically hybridizes to such a polynucleotide. The kit may optionally provide additional components that are useful in the procedure, including, but not limited to, buffers, developing reagents, labels, reacting surfaces, means for detection, control samples, standards, instructions, and interpretive information.

Detecting a polypeptide encoded by a polynucleotide that is differentially expressed in a colon cancer cell

[0083] In some embodiments, methods are provided for a colon cancer cell by detecting in the cell a polypeptide encoded by a gene differentially expressed in a colon cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, immunoassay, using antibody specific for the encoded polypeptide, e.g., by enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and the like; and functional assays for the encoded polypeptide, e.g., binding activity or enzymatic activity.

[0084] For example, an immunofluorescence assay can be easily performed on cells without first isolating the encoded polypeptide. The cells are first fixed onto a solid support, such as a microscope slide or microtiter well. This fixing step can permeabilize the cell membrane. The permeablization of the cell membrane permits the polypeptide-specific probe (*e.g*, antibody) to bind. Alternatively, where the polypeptide is secreted or membrane-bound, or is otherwise accessible at the cell-surface (*e.g.*, receptors, and other molecule stably-associated with the outer cell membrane or otherwise stably associated with the cell membrane, such permeabilization may not be necessary.

[0085] Next, the fixed cells are exposed to an antibody specific for the encoded polypeptide. To increase the sensitivity of the assay, the fixed cells may be further exposed to a second antibody, which is labeled and binds to the first antibody, which is specific for the encoded polypeptide. Typically, the secondary antibody is detectably labeled, e.g., with a fluorescent marker. The cells which express the encoded polypeptide will be fluorescently labeled and easily visualized under the microscope. See, for example, Hashido et al. (1992) *Biochem. Biophys. Res. Comm.* 187:1241-1248.

[0086] As will be readily apparent to the ordinarily skilled artisan upon reading the present specification, the detection methods and other methods described herein can be readily varied. Such variations are within the intended scope of the invention. For example, in the above detection scheme, the probe for use in detection can be immobilized on a solid support, and the test sample contacted with the immobilized probe. Binding of the test sample to the probe can then be detected in a variety of ways, *e.g.*, by detecting a detectable label bound to the test sample to facilitate detected of test sample-immobilized probe complexes.

[0087] The present invention further provides methods for detecting the presence of and/or measuring a level of a polypeptide in a biological sample, which polypeptide is encoded by a polynucleotide that represents a gene differentially expressed in cancer, particularly in a colon cancer cell, using a probe specific for the encoded polypeptide. In this embodiment, the probe can be a an antibody or other polypeptide, peptide, or molecule (*e.g.*, receptor ligand) that specifically binds a target polypeptide of interest.

[0088] The methods generally comprise: a) contacting the sample with an antibody specific for a differentially expressed polypeptide in a test cell; and b) detecting binding between the antibody and molecules of the sample. The level of antibody binding (either qualitative or quantitative) indicates the cancerous state of the cell. For example, where the differentially expressed gene is increased in cancerous cells, detection of an increased level of antibody binding to the test sample relative to antibody binding level associated with a normal cell indicates that the test cell is cancerous.

[0089] Suitable controls include a sample known not to contain the encoded polypeptide; and a sample contacted with an antibody not specific for the encoded polypeptide, e.g., an anti-idiotype antibody. A variety of methods to detect specific antibody-antigen

interactions are known in the art and can be used in the method, including, but not limited to, standard immunohistological methods, immunoprecipitation, an enzyme immunoassay, and a radioimmunoassay.

[0090] In general, the specific antibody will be detectably labeled, either directly or indirectly. Direct labels include radioisotopes; enzymes whose products are detectable (e.g., luciferase, ∃-galactosidase, and the like); fluorescent labels (e.g., fluorescein isothiocyanate, rhodamine, phycoerythrin, and the like); fluorescence emitting metals, e.g., ^{152}Eu, or others of the lanthanide series, attached to the antibody through metal chelating groups such as EDTA; chemiluminescent compounds, e.g., luminol, isoluminol, acridinium salts, and the like; bioluminescent compounds, e.g., luciferin, aequorin (green fluorescent protein), and the like.

[0091] The antibody may be attached (coupled) to an insoluble support, such as a polystyrene plate or a bead. Indirect labels include second antibodies specific for antibodies specific for the encoded polypeptide ("first specific antibody"), wherein the second antibody is labeled as described above; and members of specific binding pairs, e.g., biotin-avidin, and the like. The biological sample may be brought into contact with and immobilized on a solid support or carrier, such as nitrocellulose, that is capable of immobilizing cells, cell particles, or soluble proteins. The support may then be washed with suitable buffers, followed by contacting with a detectably-labeled first specific antibody. Detection methods are known in the art and will be chosen as appropriate to the signal emitted by the detectable label. Detection is generally accomplished in comparison to suitable controls, and to appropriate standards.

[0092] In some embodiments, the methods are adapted for use *in vivo*, e.g., to locate or identify sites where colon cancer cells are present. In these embodiments, a detectably-labeled moiety, e.g., an antibody, which is specific for a colon cancer-associated polypeptide is administered to an individual (e.g., by injection), and labeled cells are located using standard imaging techniques, including, but not limited to, magnetic resonance imaging, computed tomography scanning, and the like. In this manner, colon cancer cells are differentially labeled.

Detecting a polynucleotide that represents a gene differentially expressed in a colon cancer cell

[0093] In some embodiments, methods are provided for detecting a colon cancer cell by detecting expression in the cell of a transcript or that is differentially expressed in a colon cancer cell. Any of a variety of known methods can be used for detection, including, but not limited to, detection of a transcript by hybridization with a polynucleotide that hybridizes to a polynucleotide that is differentially expressed in a colon cancer cell; detection of a transcript by a polymerase chain reaction using specific oligonucleotide primers; *in situ* hybridization of a cell using as a probe a polynucleotide that hybridizes to a gene that is differentially expressed in a colon cancer cell.

[0094] The methods can be used to detect and/or measure mRNA levels of a gene that is differentially expressed in a colon cancer cell. In some embodiments, the methods comprise: a) contacting a sample with a polynucleotide that corresponds to a differentially expressed gene described herein under conditions that allow hybridization; and b) detecting hybridization, if any. Detection of differential hybridization, when compared to a suitable control, is an indication of the presence in the sample of a polynucleotide that is differentially expressed in a colon cancer cell. Appropriate controls include, for example, a sample which is known not to contain a polynucleotide that is differentially expressed in a colon cancer cell, and use of a labeled polynucleotide of the same "sense" as the polynucleotide that is differentially expressed in a colon cancer cell . Conditions that allow hybridization are known in the art, and have been described in more detail above.

[0095] Detection can also be accomplished by any known method, including, but not limited to, *in situ* hybridization, PCR (polymerase chain reaction), RT-PCR (reverse transcription-PCR), and "Northern" or RNA blotting, or combinations of such techniques, using a suitably labeled polynucleotide. A variety of labels and labeling methods for polynucleotides are known in the art and can be used in the assay methods of the invention. Specific hybridization can be determined by comparison to appropriate controls.

[0096] . Polynucleotide generally comprising at least 12 contiguous nt of a polynucleotide provided herein, as shown in the Sequence Listing or of the sequences of the genes

corresponding to the polynucleotides of the Sequence Listing, are used for a variety of purposes, such as probes for detection of and/or measurement of, transcription levels of a polynucleotide that is differentially expressed in a colon cancer cell. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences. It should be noted that "probe" as used in this context of detection of nucleic acid is meant to refer to a polynucleotide sequence used to detect a differentially expressed gene product in a test sample. As will be readily appreciated by the ordinarily skilled artisan, the probe can be detectably labeled and contacted with, for example, an array comprising immobilized polynucleotides obtained from a test sample (*e.g.*, mRNA). Alternatively, the probe can be immobilized on an array and the test sample detectably labeled. These and other variations of the methods of the invention are well within the skill in the art and are within the scope of the invention.

[0097] Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization can be quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluorophoress, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

[0098] PCR is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al.*, *Meth. Enzymol.* (1987) *155*:335; USPN 4,683,195; and USPN 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the

complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected.

[0099] Methods using PCR amplification can be performed on the DNA from a single cell, although it is convenient to use at least about 10^5 cells. The use of the polymerase chain reaction is described in Saiki et al. (1985) *Science* 239:487, and a review of current techniques may be found in Sambrook, *et al.* Molecular Cloning: A Laboratory Manual, CSH Press 1989, pp.14.2-14.33. A detectable label may be included in the amplification reaction. Suitable detectable labels include fluorochromes,(*e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.* ^{32}P, ^{35}S, ^{3}H, *etc.*), and the like. The label may be a two stage system, where the polynucleotides is conjugated to biotin, haptens, *etc.* having a high affinity binding partner, *e.g.* avidin, specific antibodies, *etc.*, where the binding partner is conjugated to a detectable label. The label may be conjugated to one or both of the primers. Alternatively, the pool of nucleotides used in the amplification is labeled, so as to incorporate the label into the amplification product.

Arrays

[00100] Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotides or polypeptides in a sample. This technology can be used as a tool to test for differential expression.

[00101] A variety of methods of producing arrays, as well as variations of these methods, are known in the art and contemplated for use in the invention. For example, arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions.

[00102] Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Alternatively, the polynucleotides of the test sample can be immobilized on the array, and the probes detectably labeled. Techniques for constructing arrays and methods of using these arrays are described in, for example, Schena et al. (1996) Proc Natl Acad Sci U S A. 93(20):10614-9; Schena et al. (1995) Science 270(5235):467-70; Shalon et al. (1996) Genome Res. 6(7):639-45, USPN 5,807,522, EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734.

[00103] Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a gene corresponding to a polynucleotide described herein, where expression is compared between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) *8*:217; and Ramsay *Nature Biotechnol.* (1998) *16*:40. Furthermore, many variations on methods of detection using arrays are well within the skill in the art and within the scope of the present invention. For example, rather than immobilizing the probe to a solid support, the test sample can be immobilized on a solid support which is then contacted with the probe.

DIAGNOSIS, PROGNOSIS, ASSESSMENT OF THERAPY (THERAMETRICS), AND MANAGEMENT OF CANCER

[00104] The polynucleotides described herein, as well as their gene products and corresponding genes and gene products, are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions.

[00105] For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting, antagonists (*e.g.*, small molecules), and gene therapy.

[00106] Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the genes corresponding to the polynucleotides described herein are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

[00107] The polynucleotides that correspond to differentially expressed genes, as well as their encoded gene products, can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. In addition, the polynucleotides described herein, as well as the genes corresponding to such polynucleotides, can be useful as therametrics, *e.g.*, to assess the effectiveness of therapy by using the polynucleotides or their encoded gene products, to assess, for example, tumor burden in the patient before, during, and after therapy.

[00108] Furthermore, a polynucleotide identified as corresponding to a gene that is differentially expressed in, and thus is important for, one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide represents a gene differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide corresponding to a gene that has clinical implications for metastatic colon cancer can also have clinical implications for breast cancer or ovarian cancer.

[00109] Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following "TNM" system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage II, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

[00110] The polynucleotides and corresponding genes and gene products described herein can facilitate fine-tuning of the staging process by identifying markers for the aggressiveness of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

[00111] Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identifyy tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor

corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors generally being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the Sequence Listing, and their corresponding genes and gene products, can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

[00112] Detection of colon cancer. The polynucleotides corresponding to genes that exhibit the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews.

[00113] The expression of appropriate polynucleotides can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more gene products of the genes corresponding to the polynucleotides described herein, and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC, ras, FAP (see, e.g., Fearon ER, *et al.*, *Cell* (1990) *61(5)*:759; Hamilton SR *et al.*, *Cancer* (1993) *72*:957; Bodmer W, *et al.*, *Nat Genet.* (1994) *4(3)*:217; Fearon ER, *Ann N Y Acad Sci.* (1995) *768*:101).

[00114] For example, development of colon cancer can be detected by examining the level of expression of a gene corresponding to a polynucleotides described herein to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc. For a review of markers of cancer, see, *e.g.*, Hanahan et al. (2000) Cell 100:57-70.

Treatment of colon cancer

[00115] The invention further provides methods for reducing growth of colon cancer cells. The methods provide for decreasing the expression of a gene that is differentially expressed in a colon cancer cell or decreasing the level of and/or decreasing an activity of a colon cancer-associated polypeptide. In general, the methods comprise contacting a colon cancer cell with a substance that modulates (1) expression of a gene that is differentially expressed in colon cancer; or (2) a level of and/or an activity of a colon cancer-associated polypeptide.

[00116] "Reducing growth of colon cancer cells" includes, but is not limited to, reducing proliferation of colon cancer cells, and reducing the incidence of a non-cancerous colon cell becoming a cancerous colon cell. Whether a reduction in colon cancer cell growth has been achieved can be readily determined using any known assay, including, but not limited to, [^{3}H]-thymidine incorporation; counting cell number over a period of time; detecting and/or measuring a marker associated with colon cancer (e.g., CEA, CA19-9, and LASA).

[00117] The present invention provides methods for treating colon cancer, generally comprising administering to an individual in need thereof a substance that reduces colon cancer cell growth, in an amount sufficient to reduce colon cancer cell growth and treat the colon cancer. Whether a substance, or a specific amount of the substance, is effective in treating colon cancer can be assessed using any of a variety of known diagnostic assays for colon cancer, including, but not limited to, sigmoidoscopy, proctoscopy, rectal examination, colonoscopy with biopsy, contrast radiographic studies, CAT scans, angiography, and detection of a tumor marker associated with colon cancer in the blood of the individual. The substance can be administered systemically or locally. Thus, in

some embodiments, the substance is administered locally, and colon cancer growth is decreased at the site of administration. Local administration may be useful in treating, e.g., a solid tumor.

[00118] A substance that reduces colon cancer cell growth can be targeted to a colon cancer cell. Thus, in some embodiments, the invention provides a method of delivering a drug to a colon cancer cell, comprising administering a drug-antibody complex to a subject, wherein the antibody is specific for a colon cancer-associated polypeptide, and the drug is one that reduces colon cancer cell growth, a variety of which are known in the art. Targeting can be accomplished by coupling (e.g., linking, directly or via a linker molecule, either covalently or non-covalently, so as to form a drug-antibody complex) a drug to an antibody specific for a colon cancer-associated polypeptide. Methods of coupling a drug to an antibody are well known in the art and need not be elaborated upon herein.

IDENTIFICATION OF THERAPEUTIC TARGETS AND ANTI-CANCER THERAPEUTIC AGENTS

[00119] The present invention also encompasses methods for identification of agents having the ability to modulate activity of a differentially expressed gene product, as well as methods for identifying a differentially expressed gene product as a therapeutic target for treatment of cancer, especially colon cancer.

Candidate agents

[00120] Identification of compounds that modulate activity of a differentially expressed gene product can be accomplished using any of a variety of drug screening techniques. Such agents are candidates for development of cancer therapies. Of particular interest are screening assays for agents that has tolerable toxicity for normal, non-cancerous human cells. The screening assays of the invention are generally based upon the ability of the agent to modulate an activity of a differentially expressed gene product and/or to inhibit or suppress phenomenon associated with cancer (*e.g.*, cell proliferation, colony formation, cell cycle arrest, metastasis, and the like).

[00121] The term "agent" as used herein describes any molecule, *e.g.* protein or pharmaceutical, with the capability of modulating a biological activity of a gene product of a differentially expressed gene. Generally a plurality of assay mixtures are run in

parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, *i.e.* at zero concentration or below the level of detection.

[00122] Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including, but not limited to: peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

[00123] Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts (including extracts from human tissue to identify endogenous factors affecting differentially expressed gene products) are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, *etc.* to produce structural analogs.

[00124] Exemplary candidate agents of particular interest include, but are not limited to, antisense polynucleotides, and antibodies, soluble receptors, and the like. Antibodies and soluble receptors are of particular interest as candidate agents where the target differentially expressed gene product is secreted or accessible at the cell-surface (*e.g.*, receptors and other molecule stably-associated with the outer cell membrane).

Screening of candidate agents

[00125] Screening assays can be based upon any of a variety of techniques readily available and known to one of ordinary skill in the art. In general, the screening assays involve contacting a cancerous cell (preferably a cancerous colon cell) with a candidate agent, and assessing the effect upon biological activity of a differentially expressed gene product. The effect upon a biological activity can be detected by, for example, detection of expression of a gene product of a differentially expressed gene (*e.g.*, a decrease in mRNA or polypeptide levels, would in turn cause a decrease in biological activity of the gene product). Alternatively or in addition, the effect of the candidate agent can be assessed by examining the effect of the candidate agent in a functional assay. For example, where the differentially expressed gene product is an enzyme, then the effect upon biological activity can be assessed by detecting a level of enzymatic activity associated with the differentially expressed gene product. The functional assay will be selected according to the differentially expressed gene product. In general, where the differentially expressed gene is increased in expression in a cancerous cell, agents of interest are those that decrease activity of the differentially expressed gene product.

[00126] Assays described infra can be readily adapted in the screening assay embodiments of the invention. Exemplary assays useful in screening candidate agents include, but are not limited to, hybridization-based assays (*e.g.*, use of nucleic acid probes or primers to assess expression levels), antibody-based assays (*e.g.*, to assess levels of polypeptide gene products), binding assays (*e.g.*, to detect interaction of a candidate agent with a differentially expressed polypeptide, which assays may be competitive assays where a natural or synthetic ligand for the polypeptide is available), and the like. Additional exemplary assays include, but are not necessarily limited to, cell proliferation assays, antisense knockout assays, assays to detect inhibition of cell cycle, assays of induction of cell death/apoptosis, and the like. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an animal model of the cancer.

Identification of therapeutic targets

[00127] In another embodiment, the invention contemplates identification of differentially expressed genes and gene products as therapeutic targets. In some respects, this is the converse of the assays described above for identification of agents having activity in

modulating (*e.g.*, decreasing or increasing) activity of a differentially expressed gene product.

[00128] In this embodiment, therapeutic targets are identified by examining the effect(s) of an agent that can be demonstrated or has been demonstrated to modulate a cancerous phenotype (*e.g.*, inhibit or suppress or prevent development of a cancerous phenotype). Such agents are generally referred to herein as an "anti-cancer agent", which agents encompass chemotherapeutic agents. For example, the agent can be an antisense oligonucleotide that is specific for a selected gene transcript. For example, the antisense oligonucleotide may have a sequence corresponding to a sequence of a differentially expressed gene described herein, *e.g.*, a sequence of one of SEQ ID NOS:1-309.

[00129] Assays for identification of therapeutic targets can be conducted in a variety of ways using methods that are well known to one of ordinary skill in the art. For example, a test cancerous cell that expresses or overexpresses a differentially expressed gene is contacted with an anti-cancer agent, the effect upon a cancerous phenotype and a biological activity of the candidate gene product assessed. The biological activity of the candidate gene product can be assayed be examining, for example, modulation of expression of a gene encoding the candidate gene product (*e.g.*, as dectected by, for example, an increase or decrease in transcript levels or polypeptide levels), or modulation of an enzymatic or other activity of the gene product. The cancerous phenotype can be, for example, cellular proliferation, loss of contact inhibition of growth (*e.g.*, colony formation), tumor growth (*in vitro* or *in vivo*), and the like. Alternatively or in addition, the effect of modulation of a biological activity of the candidate target gene upon cell death/apoptosis or cell cycle regulation can be assessed.

[00130] Inhibition or suppression of a cancerous phenotype, or an increase in cell/death apoptosis as a result of modulation of biological activity of a candidate gene product indicates that the candidate gene product is a suitable target for cancer therapy. Assays described infra can be readily adapted in for assays for identification of therapeutic targets. Generally such assays are conducted *in vitro*, but many assays can be adapted for *in vivo* analyses, *e.g.*, in an appropriate, art-accepted animal model of the cancer.

USE OF POLYPEPTIDES TO SCREEN FOR PEPTIDE ANALOGS AND ANTAGONISTS

[00131] Polypeptides encoded by differentially expressed genes identified herein can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, e.g., USPN 5,010,175 , and WO 91/17823).

[00132] Agonists or antagonists of the polypeptides if the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

[00133] Such screening and experimentation can lead to identification of a polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide described herein, and at least one peptide agonist or antagonist of the binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

PHARMACEUTICAL COMPOSITIONS AND USES

[00134] Pharmaceutical compositions can comprise polypeptides, receptors that specifically bind a polypeptide produced by a differentially expressed gene (*e.g.*, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The compositions can be used to treat primary tumors as well as metastases of primary tumors. In addition, the

pharmaceutical compositions can be used in conjunction with conventional methods of cancer treatment, *e.g.*, to sensitize tumors to radiation or conventional chemotherapy.

[00135] Where the pharmaceutical composition comprises a receptor (such as an antibody) that specifically binds to a gene product encoded by a differentially expressed gene, the receptor can be coupled to a drug for delivery to a treatment site or coupled to a detectable label to facilitate imaging of a site comprising colon cancer cells. Methods for coupling antibodies to drugs and detectable labels are well known in the art, as are methods for imaging using detectable labels.

[00136] The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature.

[00137] The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

[00138] A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such

as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles.

[00139] Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington: The Science and Practice of Pharmacy* (1995) Alfonso Gennaro, Lippincott, Williams, & Wilkins.

DELIVERY METHODS

[00140] Once formulated, the compositions contemplated by the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide, polypeptides, small molecule agonists or antagonists, and the like); or (2) delivered ex vivo, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

[00141] Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation,

encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

[00142] Once differential expression of a gene corresponding to a polynucleotide described herein has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.). In other embodiments, the disorder can be amenable to treatment by administration of a small molecule drug that, for example, serves as an inhibitor (antagonist) of the function of the encoded gene product of a gene having increased expression in cancerous cells relative to normal cells or as an agonist for gene products that are decreased in expression in cancerous cells (*e.g.*, to promote the activity of gene products that act as tumor suppressors).

[00143] The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic compositions agents includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. In general, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

[00144] Targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) *11*:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) *263*:621; Wu *et al.*, *J. Biol. Chem.* (1994) *269*:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) *87*:3655; Wu *et al.*, *J. Biol. Chem.* (1991) *266*:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μg to about 2 mg, about 5 μg to about 500 μg, and about 20 μg to about 100 :g of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides.

[00145] Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

[00146] The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) *1*:51; Kimura, *Human Gene Therapy* (1994) *5*:845; Connelly, *Human Gene Therapy* (1995) *1*:185; and Kaplitt, *Nature Genetics* (1994) *6*:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

[00147] Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) *3*:147 can also be employed.

[00148] Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) *3*:147); ligand-linked DNA(see, e.g., Wu, *J. Biol. Chem.* (1989) *264*:16985); eukaryotic cell delivery vehicles cells (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN 5,580,859. Liposomes that can act as gene delivery vehicles are described in USPN 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) *14*:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) *91*:1581.

[00149] Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) *91*(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., USPN 5,206,152 and

WO 92/11033).

EXAMPLES

[00150] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

EXAMPLE 1: SOURCE OF BIOLOGICAL MATERIALS AND ISOLATION OF POLYNUCLEOTIDES EXPRESSED BY THE BIOLOGICAL MATERIALS

[00151] Candidate polynucleotides that may represent genes differentially expressed in cancer were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. In order to obtain the latter polynucleotides, mRNA was isolated from several selected cell lines and patient tissues, and used to construct cDNA libraries. The cells and tissues that served as sources for these cDNA libraries are summarized in Table 1 below.

Table 1. Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in Library
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High	223620

Library (lib #)	Description	Number of Clones in Library
	Metastatic Potential	
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMVEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMVEC) – bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMVEC) – VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon – UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	248436
16	Colon Tumor – UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	263206
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	266482
18	Normal Colon – UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor – UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306197
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349

[00152] The human colon cancer cell line Km12L4-A (Morikawa, et al., *Cancer Research* (1988) *48*:6863) is derived from the KM12C cell line. The KM12C cell line (Morikawa et al. *Cancer Res.* (1988) *48*:1943-1948), which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B_2 surgical specimen (Morikawa *et al. Cancer Res.* (1988) *48*:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman *et al. Nucl. Acids. Res.* (1995) *23*:4007; Bao-Ling *et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) *21*:3269). The KM12C and KM12C-derived cell lines (*e.g.*, KM12L4, KM12L4-A, *etc.*) are well-recognized in the art as a model cell line for the

study of colon cancer (see, *e.g.*, Moriakawa *et al.*, *supra*; Radinsky *et al. Clin. Cancer Res.* (1995) *1*:19; Yeatman *et al.*, (1995) *supra*; Yeatman *et al. Clin. Exp. Metastasis* (1996) *14*:246).

[00153] The MDA-MB-231 cell line (Brinkley et al. *Cancer Res.* (1980) *40*:3118-3129) was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) *53*:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, *e.g.*, Chandrasekaran *et al.*, *Cancer Res.* (1979) *39*:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) *41*:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) *77*:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) *26*:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) *40*:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) *11*:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) *10*:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) *15*:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) *8*:696 (MV522)).

[00154] The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cell lines were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

Characterization of sequences in the libraries

[00155] The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular

Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. Masking resulted in the elimination of several sequences. The remaining sequences were then used in a BLASTN vs. GenBank search. Gene assignment for the query sequences was determined based on best hit from the GenBank database; expectancy values are provided with the hit.

Summary of polynucleotides described herein

[00156] Table 2 (inserted before the claims) provides a summary of polynucleotides isolated as described above and identified as corresponding to a differentially expressed gene (see Example 2 below), as well as those polynucleotides obtained from publicly available sources. Specifically, Table 2 provides: 1) the SEQ ID NO assigned to each sequence for use in the present specification; 2) the Candidate Identification Number ("CID") to which the sequence is assigned and which number is based on the selection of the candidate for further evaluation in the differential expression in cancerous cells relative to normal cells; 3) the Sequence Name assigned to each sequence; and 4) the name assigned to the sample or clone from which the sequence was isolated. The sequences corresponding to SEQ ID NOS are provided in the Sequence Listing. Because at least some of the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides may represent different regions of the same mRNA transcript and the same gene and/or may be contained within the same clone. Thus, if two or more SEQ ID NOS are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene. It should be noted that not all cDNA libraries described above are represented on an array in the examples described below.

Summary of Blast Search Results

[00157] Table 3 (inserted before the claims) provides the results of BLASTN searches of the Genbank database using the sequences of the polynucleotides as described above.

Table 3 includes 1) the SEQ ID NO; 2) the "CID" or Candidate Identification Number to which the sequence is assigned; 3) the GenBank accession number of the Blast hit; 4) a description of the gene encoded by the Blast hit ("HitDesc") having the closest sequence homology to the sequence on the array (and in some instances contains a sequence identical to the sequence on the array); 5) the Blast score ("Score"), which value is obtained by adding the similarities and differences of an alignment between the sequence and a database sequence, wherein a "match" is a positive value and a "mismatch" or "non-match" is a negative value; 6) the "Length" of the sequence, which represents the number of nucleotides in the database "hit"; 7) the Expect value (E) which describes the number of hits or matches "expected" if the database was random sequence, i.e. the E value describes the random background noise that exists for matches between sequences; and 8) the "Identities" ratio which is a ratio of number of bases in the query sequence that exactly match the number of bases in the database sequence when aligned.

EXAMPLE 2: DETECTION OF DIFFERENTIAL EXPRESSION USING ARRAYS

[00158] mRNA isolated from samples of cancerous and normal colon tissue obtained from patients were analyzed to identify genes differentially expressed in cancerous and normal cells. Normal and cancerous cells collected from cryopreserved patient tissues were isolated using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, *e.g.*, Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001).

[00159] Table 4 (inserted before the claims) provides information about each patient from which the samples were isolated, including: the "Patient ID" and "Path ReportID", which are numbers assigned to the patient and the pathology reports for identification purposes; the "Group" to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the "Primary Tumor Size"; the "Primary Tumor Grade"; the identification of the histopathological grade ("Histopath Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("Lymph Node Met"); the incidence of lymph node metastases (provided as a

number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Incidence Lymphnode Met"); the "Regional Lymphnode Grade"; the identification or detection of metastases to sites distant to the tumor and their location ("Distant Met & Loc"); a description of the distant metastases ("Descrip Distant Met"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Adenoma was not described in any of the patients; adenoma dysplasia (described as hyperplasia by the pathologist) was described in Patient ID No. 695. Extranodal extensions were described in two patients, Patient ID Nos. 784 and 791. Lymphovascular invasion was described in seven patients, Patient ID Nos. 128, 278, 517, 534, 784, 786, and 791. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Identification of differentially expressed genes

[00160] cDNA probes were prepared from total RNA isolated from the patient cells described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

[00161] Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

[00162] Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.

[00163] Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array.

[00164] Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample.

[00165] Table 5 (inserted before the claims) describes the physical location of the differentially expressed polynucleotides on the arrays. Table 5 includes: 1) a Spot ID, which is a unique identifier for each spot containing target sequence of interest on all arrays used; 2) a "Chip Num" which refers to a particular array representing a specific set of genes; 3) the "Sample Name or Clone Name" from which the sequence was obtained; and 4) the coordinates of the sequence on the particular array ("Coordinates"). Table 9 (inserted before the claims) provides information about the sequences on the arrays, specifically: 1) Candidate Identification Number; 2) Sample name or clone name; 3) function of the gene corresponding to the sequence (as determined by homology to genes of known function by BLAST search of GenBank); 4) the class of the gene (as determined by homology to genes of known function by BLAST search of GenBank); 5) the pathway in which the gene is implicated; 6) gene assignment; which refers to the gene to which the sequence has the greatest homology or identity; 7) the "Gene Symbol"; 8) chromosome number on which the gene is located ("Chrom Num"); 9) the map position on the chromosome.

[00166] The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

[00167] The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

[00168] The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

[00169] A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial

analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p>0.05$).

[00170] Table 6 (inserted before the claims) provides the results for gene products differentially expressed in the colon tumor samples relative to normal tissue samples. Table 6 includes: 1) the SEQ ID NO; 2) the CID or candidate identification number; 3) the spot identification number ("SpotID"); 4) the percentage of patients tested in which expression levels of the gene was at least 2-fold greater in cancerous tissue than in matched normal tissue (">=2x"); 5) the percentage of patients tested in which expression levels of the gene was at least 2.5-fold greater in cancerous tissue than in matched normal tissue (">=2.5x"); 6) the percentage of patients tested in which expression levels of the gene was at least 5-fold greater in cancerous tissue than in matched normal cells (">=5x"); 7) the percentage of patients tested in which expression levels of the gene was less than or equal to ½ of the expression level in matched normal cells ("<=halfx"); and 8) the number of patients tested for each sequence. Table 6 also includes the results from each patient, identified by the patient ID number (*e.g.*, 15Ratio). This data represents the ratio of differential expression for the samples tested from that particular patient's tissues (*e.g.*, "15Ratio" is the ratio from the tissue samples of patient ID no. 15). The ratios of differential expression is expressed as a normalized hybridization signal associated with the tumor probe divided by the normalized hybridization signal with the normal probe. Thus, a ratio greater than 1 indicates that the gene product is increased in expression in cancerous cells relative to normal cells, while a ratio of less than 1 indicates the opposite.

[00171] These data provide evidence that the genes represented by the polynucleotides having the indicated sequences are differentially expressed in colon cancer.

EXAMPLE 3: ANTISENSE REGULATION OF GENE EXPRESSION

[00172] The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells was analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

[00173] A number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein were designed as potential antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target were designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh, RNAture, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors considered when designing antisense oligonucleotides include: 1) the secondary structure of oligonucleotides; 2) the secondary structure of the target gene; 3) the specificity with no or minimum cross-hybridization to other expressed genes; 4) stability; 5) length and 6) terminal GC content. The antisense oligonucleotide is designed to so that it will hybridize to its target sequence under conditions of high stringency at physiological temperatures (*e.g.*, an optimal temperature for the cells in culture to provide for hybridization in the cell, e.g., about 37°C), but with minimal formation of homodimers.

[00174] Using the sets of oligomers and the HYBsimulator program, three to ten antisense oligonucleotides and their reverse controls were designed and synthesized for each candidate mRNA transcript, which transcript was obtained from the gene corresponding to the target polynucleotide sequence of interest. Once synthesized and quantitated, the oligomers were screened for efficiency of a transcript knock-out in a panel of cancer cell lines. The efficiency of the knock-out was determined by analyzing mRNA levels using lightcycler quantification. The oligomers that resulted in the highest level of transcript knock-out, wherein the level was at least about 50%, preferably about 80-90%, up to 95% or more up to undetectable message, were selected for use in a cell-based proliferation assay, an anchorage independent growth assay, and an apoptosis assay.

[00175] The ability of each designed antisense oligonucleotide to inhibit gene expression was tested through transfection into SW620 colon colorectal carcinoma cells. For each transfection mixture, a carrier molecule, preferably a lipitoid or cholesteroid, was prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μm PVDF membrane. The antisense or control oligonucleotide was then prepared to a working concentration of 100 μM in sterile Millipore water. The oligonucleotide was further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 μM, or approximately 20 μg oligo/ml of OptiMEM™. In a separate microfuge tube, lipitoid or cholesteroid, typically in the amount of about 1.5-2 nmol lipitoid/μg antisense oligonucleotide, was diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide was immediately added to the diluted lipitoid and mixed by pipetting up and down. Oligonucleotide was added to the cells to a final concentration of 30 nM.

[00176] The level of target mRNA that corresponds to a target gene of interest in the transfected cells was quantitated in the cancer cell lines using the Roche LightCycler™ real-time PCR machine. Values for the target mRNA were normalized versus an internal control (*e.g.*, beta-actin). For each 20 μl reaction, extracted RNA (generally 0.2-1 μg total) was placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water was added to a total volume of 12.5 μl. To each tube was added 7.5 μl of a buffer/enzyme mixture, prepared by mixing (in the order listed) 2.5 μl H_2O, 2.0 μl 10X reaction buffer, 10 μl oligo dT (20 pmol), 1.0 μl dNTP mix (10 mM each), 0.5 μl RNAsin® (20u) (Ambion, Inc., Hialeah, FL), and 0.5 μl MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents were mixed by pipetting up and down, and the reaction mixture was incubated at 42°C for 1 hour. The contents of each tube were centrifuged prior to amplification.

[00177] An amplification mixture was prepared by mixing in the following order: 1X PCR buffer II, 3 mM $MgCl_2$, 140 μM each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H_2O to 20 μl. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene, OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the

fluorescence from SYBR® Green increases. To each 20 µl aliquot of amplification mixture, 2 µl of template RT was added, and amplification was carried out according to standard protocols.

[00178] The results of the antisense assays are provided in Table 7 (inserted before the claims). The results are expressed as the percent decrease in expression of the corresponding gene product relative to non-transfected cells, vehicle-only transfected (mock-transfected) cells, or cells transfected with reverse control oligonucleotides. Table 7 includes: 1) the SEQ ID NO; 2) the CID; 3) the "Gene Assignment" which refers to the gene to which the sequence has the greatest homology or identity; 4) the "Gene Symbol"; 5) GenBank gene name; and 6) the percent decrease in expression of the gene relative to control cells ("mRNA KO").

EXAMPLE 4: EFFECT OF EXPRESSION ON PROLIFERATION

[00179] The effect of gene expression on the inhibition of cell proliferation was assessed in metastatic breast cancer cell lines (MDA-MB-231 ("231")), SW620 colon colorectal carcinoma cells, or SKOV3 cells (a human ovarian carcinoma cell line).

[00180] Cells were plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide was diluted to 2 µM in OptiMEM™ and added to OptiMEM™ into which the delivery vehicle, lipitoid 116-6 in the case of SW620 cells or 1:1 lipitoid 1:cholesteroid 1 in the case of MDA-MB-231 cells, had been diluted. The oligo/delivery vehicle mixture was then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments was 300 nM, and the final ratio of oligo to delivery vehicle for all experiments was 1.5 nmol lipitoid/µg oligonucleotide.

[00181] Antisense oligonucleotides were prepared as described above (see Example 3). Cells were transfected overnight at 37°C and the transfection mixture was replaced with fresh medium the next morning. Transfection was carried out as described above in Example 3.

[00182] The results of the antisense experiments are shown in Table 8 (inserted before the claims, column labeled "Proliferation"). Those antisense oligonucleotides that resulted in decreased proliferation in SW620 colorectal carcinoma cells are indicated by "Inhib in "

and "weak effect in", with the cell type following. Those antisense oligonucleotides that resulted in inhibition of proliferation of SW620 cells indicates that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibited proliferation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that resulted in inhibition of proliferation of MDA-MB-231 cells indicates that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells.

EXAMPLE 5: EFFECT OF GENE EXPRESSION ON COLONY FORMATION

[00183] The effect of gene expression upon colony formation of SW620 cells, SKOV3 cells, and MD-MBA-231 cells was tested in a soft agar assay. Soft agar assays were conducted by first establishing a bottom layer of 2 ml of 0.6% agar in media plated fresh within a few hours of layering on the cells. The cell layer was formed on the bottom layer by removing cells transfected as described above from plates using 0.05% trypsin and washing twice in media. The cells were counted in a Coulter counter, and resuspended to 10^6 per ml in media. 10 µl aliquots were placed with media in 96-well plates (to check counting with WST1), or diluted further for the soft agar assay. 2000 cells were plated in 800 µl 0.4% agar in duplicate wells above 0.6% agar bottom layer. After the cell layer agar solidified, 2 ml of media was dribbled on top and antisense or reverse control oligo (produced as described in Example 3) was added without delivery vehicles. Fresh media and oligos were added every 3-4 days. Colonies formed in 10 days to 3 weeks. Fields of colonies were counted by eye. Wst-1 metabolism values can be used to compensate for small differences in starting cell number. Larger fields can be scanned for visual record of differences.

[00184] Table 8 (inserted before the claims) provides the results of these assays ("Softagar"). Those antisense oligonucleotides that resulted in inhibition of colony formation are indicated by "inhibits", "weak effect", or "weak inhibition" followed by the cell type. Those antisense oligonucleotides that resulted in inhibition of colony formation of SW620 cells indicates that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense

oligonucleotides that inhibited colony formation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that resulted in inhibition of colony formation of MDA-MB-231 cells indicates that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells.

EXAMPLE 6: INDUCTION OF CELL DEATH UPON DEPLETION OF POLYPEPTIDES BY DEPLETION OF MRNA ("ANTISENSE KNOCKOUT")

[00185] In order to assess the effect of depletion of a target message upon cell death, SW620 cells, or other cells derived from a cancer of interest, are transfected for proliferation assays. For cytotoxic effect in the presence of cisplatin (cis), the same protocol is followed but cells are left in the presence of 2 μM drug. Each day, cytotoxicity was monitored by measuring the amount of LDH enzyme released in the medium due to membrane damage. The activity of LDH is measured using the Cytotoxicity Detection Kit from Roche Molecular Biochemicals. The data is provided as a ratio of LDH released in the medium vs. the total LDH present in the well at the same time point and treatment (rLDH/tLDH). A positive control using antisense and reverse control oligonucleotides for BCL2 (a known anti-apoptotic gene) is included; loss of message for BCL2 leads to an increase in cell death compared with treatment with the control oligonucleotide (background cytotoxicity due to transfection).

EXAMPLE 7: FUNCTIONAL ANALYSIS OF GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN COLON CANCER IN PATIENTS

[00186] The gene products of sequences of a gene differentially expressed in cancerous cells can be further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype. For example, the function of gene products corresponding to genes identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted or associated with a cell surface membrane, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the

context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype.

[00187] Where the gene product of the differentially expressed genes identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecules that inhibit or enhance function of the corresponding protein or protein family.

[00188] Additional functional assays include, but are not necessarily limited to, those that analyze the effect of expression of the corresponding gene upon cell cycle and cell migration. Methods for performing such assays are well known in the art.

EXAMPLE 8: CONTIG ASSEMBLY AND ADDITIONAL GENE CHARACTERIZATION

[00189] The sequences of the polynucleotides provided in the present invention can be used to extend the sequence information of the gene to which the polynucleotides correspond (*e.g.*, a gene, or mRNA encoded by the gene, having a sequence of the polynucleotide described herein). This expanded sequence information can in turn be used to further characterize the corresponding gene, which in turn provides additional information about the nature of the gene product (*e.g.*, the normal function of the gene product). The additional information can serve to provide additional evidence of the gene product's use as a therapeutic target, and provide further guidance as to the types of agents that can modulate its activity.

[00190] In one example, a contig was assembled using the sequence of the polynucleotide having SEQ ID NO:2 (sequence name 019.G3.sp6_128473), which is present in clone M00006883D:H12. A "contig" is a contiguous sequence of nucleotides that is assembled from nucleic acid sequences having overlapping (*e.g.*, shared or substantially similar) sequence information. The sequences of publicly-available ESTs (Expressed Sequence Tags) and the sequences of various clones from several cDNA libraries synthesized at Chiron were used in the contig assembly. None of the sequences from these latter clones

from the cDNA libraries had significant hits against known genes with function when searched using BLASTN against GenBank as described above.

[00191] The contig was assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions. The final contig was assembled from 11 sequences, provided in the Sequence Listing as SEQ ID NOS:2 and 310-320. The sequence names and SEQ ID NOS of the sequences are provided in the overview alignment produced by Sequencher (see Fig. 1).

[00192] The clone containing the sequence of 035JN032.H09 (SEQ ID NO:319) is of particular interest. This clone was originally obtained from a normalized cDNA library prepared from a prostate cancer tissue sample that was obtained from a patient with Gleason grade 3+3. The clone having the 035JN032.H09 sequence corresponds to a gene that has increased expression in (*e.g.*, is upregulated) in colon cancer as detected by microarray analysis using the protocol and materials described above. The data is provided in the table below.

SEQ ID NO	Spot ID	Chip #	Sample ID	Number of patients used to calculate concordance	% >=2x	% >=5x
2	1833	1	M00006883D:H12	33	61	33
319	27454	5	035JN032.H09	28	61	11

[00193] "% >2X" and "%>5X" indicate the percentage of patients in which the corresponding gene was expressed at two-fold and five-fold greater levels in cancerous cells relative to normal cells, respectively.

[00194] This observation thus further validates the expression profile of the clone having the sequence of 035JN032.H09, as it indicates that the gene represented by this sequence and clone is differentially expressed in at least two different cancer types.

[00195] The sequence information obtained in the contig assembly described above was used to obtain a consensus sequence derived from the contig using the Sequencher program. The consensus sequence is provided as SEQ ID NO:320 in the Sequence Listing.

[00196] In preliminary experiments, the consensus sequence was used as a query sequence in a BLASTN search of the DGTI DoubleTwist Gene Index (DoubleTwist, Inc., Oakland, CA), which contains all the EST and non-redundant sequence in public databases. This preliminary search indicated that the consensus sequence has homology to a predicted gene homologue to human atrophin-1 (HSS0190516.1 dtgic|HSC010416.3 Similar to: DRPL_HUMAN gi|17660|sp|P54259|DRPL_HUMAN ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN) [Homo sapiens (Human), provided as SEQ ID NO:322), with a Score = 1538 bits (776), Expect = 0.0, and Identities = 779/780 (99%).

[00197] While the preliminary results regarding the homology to atrophin-1 are not yet confirmed, this example, through contig assembly and the use of homology searching software programs, shows that the sequence information provided herein can be readily extended to confirm, or confirm a predicted, gene having the sequence of the polynucleotides described in the present invention. Further the information obtained can be used to identify the function of the gene product of the gene corresponding to the polynucleotides described herein. While not necessary to the practice of the invention, identification of the function of the corresponding gene, can provide guidance in the design of therapeutics that target the gene to modulate its activity and modulate the cancerous phenotype (*e.g.*, inhibit metastasis, proliferation, and the like).

[00198] While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
1	114	016824.Seq	M00003814C:C11
2	123	019.G3.sp6_128473	M00006883D:H12
3	114	020.B11.sp6_128613	M00003814C:C11
4	1	1222317	I:1222317:15A02:C02
5	2	1227385	I:1227385:14B01:G05
6	3	1297179	I:1297179:05A02:F02
7	4	1298021	I:1298021:05A01:G10
8	5	1358285	I:1358285:04A02:F11
9	6	1384823	I:1384823:01B02:F08
10	7	1395918	I:1395918:04A01:G10
11	8	1402615	I:1402615:09A02:E03
12	9	1421929	I:1421929:05A01:D02
13	10	1431819	I:1431819:14B01:D05
14	11	1443877	I:1443877:03B02:B08
15	12	1450639	I:1450639:03B02:E09
16	13	1480159	I:1480159:06B02:E03
17	14	1509602	I:1509602:04A01:A11
18	15	1516301	I:1516301:05B01:C10
19	167	1598.C19.gz43_212821	M00055583C:B07
20	16	1600586	I:1600586:05B02:F04
21	17	1609538	I:1609538:06A02:F04
22	18	1613615	I:1613615:03B01:D10
23	19	1630804	I:1630804:06A02:F10
24	20	1633286	I:1633286:06A02:E04
25	21	1666080	I:1666080:07B02:D04
26	22	1699587	I:1699587:06A02:F11
27	23	1702266	I:1702266:02B01:D09
28	24	1712592	I:1712592:04A01:E03
29	25	1723834	I:1723834:01A01:C02
30	26	1743234	I:1743234:16B01:D09
31	170	1744.K05.gz43_221934	M00056250C:B02
32	27	1749417	I:1749417:04A02:D10
33	28	1749883	I:1749883:05B01:D04
34	29	1750782	I:1750782:02A01:A08
35	30	1758241	I:1758241:15B02:G04
36	31	1809385	I:1809385:02A02:G04
37	32	1810640	I:1810640:01A02:D06
38	33	1817434	I:1817434:02B01:C02
39	34	1833191	I:1833191:14A01:G05
40	35	1854245	I:1854245:02B02:E10
41	36	1854558	I:1854558:03A01:C11
42	37	1857563	I:1857563:05B02:D01

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
43	38	1920522	I:1920522:15B02:F02
44	39	1920650	I:1920650:16A01:B01
45	41	1923490	I:1923490:18B01:H08
46	42	1923769	I:1923769:16B01:F01
47	43	1926006	I:1926006:15A01:F09
48	44	1931371	I:1931371:02B02:D12
49	45	1960722	I:1960722:13B02:D11
50	46	1963753	I:1963753:18B01:E07
51	47	1965257	I:1965257:18B02:B04
52	48	1967543	I:1967543:16B02:F06
53	49	1968921	I:1968921:15A02:D06
54	50	1969044	I:1969044:18B01:E12
56	53	1996180	I:1996180:19B01:C11
57	54	2054678	I:2054678:19A01:F10
58	55	2055926	I:2055926:14A01:F11
59	56	2056395	I:2056395:13A02:B07
60	58	2060725	I:2060725:13A01:G10
61	59	2079906	I:2079906:01A02:A06
62	60	2152363	I:2152363:04A02:A08
63	63	2239819	I:2239819:04A02:B11
64	64	2359588	I:2359588:18A01:F03
65	65	2458926	I:2458926:03B01:C07
66	66	2483109	I:2483109:05A01:A06
67	67	2499479	I:2499479:05A01:D06
68	68	2499976	I:2499976:01B02:E09
70	71	2615513	I:2615513:04B01:D09
71	74	2675481	I:2675481:05A01:G06
73	100	268.H2.sp6_144757	M00001341B:A11
74	105	270.B6.sp6_145073	M00001402B:C12
75	106	270.C6.sp6_145085	M00001402C:B01
76	104	270.H3.sp6_145142	M00001393D:F01
77	75	2759046	I:2759046:19B02:C05
78	76	2825369	I:2825369:07A02:F09
79	77	2840195	I:2840195:01B02:G11
80	78	2902903	I:2902903:12A02:F02
81	79	2914605	I:2914605:04B01:G06
82	80	2914719	I:2914719:04B02:B05
83	81	3229778	I:3229778:02B01:B07
84	109	323.B1.sp6_145452	M00001489B:G04
85	110	323.C3.sp6_145466	M00001496A:G03
86	111	324.H1.sp6_145716	M00001558C:B06
87	121	325.H11.sp6_145918	M00005360A:A07

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
88	118	325.H4.sp6_145911	M00004031B:D12
89	41	344.B2.sp6_146237	M00022742A:F08
90	139	344.C4.sp6_146251	M00023363C:A04
91	83	3518380	I:3518380:16A01:B07
92	85	4072558	I:4072558:12B01:A07
93	117	414.A11.sp6_149879	M00003961B:H05
94	113	414.F2.sp6_149930	M00001675B:G05
95	87	549299	I:549299:17B02:F06
96	88	605019	I:605019:13B02:D03
97	89	620494	I:620494:16A01:C10
98	125	626.D8.sp6_157447	M00007965C:G08
99	128	627.E8.sp6_157651	M00007987D:D04
100	127	627.G6.sp6_157673	M00007985B:A03
101	129	628.D12.sp6_157835	M00008049B:A12
102	130	634.H4.sp6_155966	M00008099D:A05
104	136	642.C6.sp6_156292	M00022168B:F02
106	5	642.D8.sp6_156306	M00022180D:E11
107	137	642.H11.sp6_156357	M00022215C:A10
108	138	653.A3.sp6_158944	M00023283C:C06
109	141	655.B4.sp6_156470	M00023431B:A01
110	90	659143	I:659143:16B01:E06
111	145	661.B5.sp6_159726	M00027066B:E09
112	91	750899	I:750899:16A01:D04
113	92	763607	I:763607:16A01:E09
114	93	901317	I:901317:16A01:G01
116	100	919.H2.SP6_168750	M00001341B:A11
118	123	956.B04.sp6_177996	M00006883D:H12
119	94	956077	I:956077:14B01:H04
120	95	970933	I:970933:14B01:D03
121	96	986558	I:986558:18A01:C09
122	98	998612	I:998612:14B02:G06
123	103	A061.ga43_378496	M00001374A:A06
124	103	A062.ga43_378497	M00001374A:A06
125	133	A121.ga43_378498	M00022009A:A12
126	133	A122.ga43_378499	M00022009A:A12
130	115	G022a.ga43_378503	M00003852B:C01
131	106	RTA00000179AF.k.22.1.Seq	M00001402C:B01
132	113	RTA00000187AF.g.2.1.Seq	M00001675B:G05
133	113	RTA00000187AR.g.2.2.Seq	M00001675B:G05
134	106	RTA00000348R.j.10.1.Seq	M00001402C:B01
135	116	RTA00000588F.l.02.2.Seq	M00003853B:G11
136	117	RTA00000588F.o.23.1.Seq	M00003961B:H05

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
138	123	RTA00000603F.d.06.1.Seq	M00006883D:H12
140	140	RTA00000847F.n.19.3.Seq	M00023371A:G03
141	143	RTA00000922F.g.12.1.Seq	M00026900D:F02
142	121	RTA00001042F.o.18.1.Seq	M00005360A:A07
143	121	RTA00001064F.c.16.1.Seq	M00005360A:A07
144	139	RTA00001069F.c.03.1.Seq	M00023363C:A04
145	112	RTA00002890F.d.16.1.P.Seq	M00001600C:B11
147	166	RTA22200002F.b.15.1.P.Seq	M00055435B:A12
148	167	RTA22200003F.b.13.1.P.Seq	M00055583C:B07
149	169	RTA22200005F.d.14.1.P.Seq	M00055873C:B06
150	30	RTA22200007F.j.17.2.P.Seq	M00056227B:G06
151	170	RTA22200007F.m.02.1.P.Sequence	M00056250C:B02
152	171	RTA22200008F.a.24.1.P.Seq	M00056301D:A04
153	171	RTA22200008F.b.01.1.P.Seq	M00056301D:A04
154	172	RTA22200008F.b.22.1.P.Sequence	M00056308A:F02
155	147	RTA22200009F.b.03.2.P.Sequence	M00042439D:C11
156	149	RTA22200009F.c.22.2.P.Seq	M00042756A:H02
157	150	RTA22200009F.e.10.1.P.Seq	M00042770D:G04
158	151	RTA22200009F.i.17.2.P.Seq	M00042818A:D05
159	173	RTA22200009F.p.21.1.P.Seq	M00056350B:B03
161	175	RTA22200010F.k.02.1.P.Seq	M00056478D:B07
162	176	RTA22200010F.k.19.1.P.Seq	M00056483D:G07
163	177	RTA22200010F.m.13.1.P.Seq	M00056500C:A07
164	178	RTA22200011F.b.05.1.P.Seq	M00056533D:G07
165	179	RTA22200011F.b.09.1.P.Seq	M00056534C:E08
166	180	RTA22200011F.g.21.1.P.Seq	M00056585B:F04
168	182	RTA22200011F.l.06.1.P.Seq	M00056619A:H02
169	183	RTA22200011F.l.15.1.P.Seq	M00056622B:F12
170	184	RTA22200011F.m.13.1.P.Seq	M00056632B:H10
171	185	RTA22200011F.n.24.1.P.Seq	M00056645C:D11
172	185	RTA22200011F.o.01.1.P.Seq	M00056645C:D11
173	186	RTA22200011F.o.03.1.P.Seq	M00056646B:F07
174	187	RTA22200012F.c.01.1.P.Seq	M00056679B:H03
176	189	RTA22200012F.f.15.1.P.Seq	M00056709B:D03
177	190	RTA22200012F.i.14.1.P.Seq	M00056728C:G02
179	192	RTA22200013F.b.20.1.P.Seq	M00056810A:A02
180	193	RTA22200013F.c.06.1.P.Seq	M00056812D:A08

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
181	194	RTA22200013F.d.15.1.P.Seq	M00056822A:E08
182	195	RTA22200013F.o.17.1.P.Seq	M00056908A:H05
183	196	RTA22200013F.p.24.1.P.Seq	M00056918C:F09
184	197	RTA22200014F.b.18.1.P.Seq	M00056937C:C10
185	197	RTA22200014F.b.18.2.P.Seq	M00056937C:C10
190	199	RTA22200014F.j.08.1.P.Seq	M00056992C:F12
191	199	RTA22200014F.j.08.2.P.Seq	M00056992C:F12
192	200	RTA22200015F.a.18.1.P.Seq	M00057044D:G03
193	176	RTA22200015F.a.23.1.P.Seq	M00057046A:G09
194	201	RTA22200015F.f.17.1.P.Seq	M00057081B:H03
196	118	RTA22200015F.k.10.1.P.Seq	M00057112B:E11
198	204	RTA22200015F.m.15.1.P.Seq	M00057127B:B09
200	206	RTA22200016F.i.21.1.P.Seq	M00057231A:G04
201	207	RTA22200016F.k.08.1.P.Seq	M00057241C:F03
202	152	RTA22200019F.h.04.1.P.Seq	M00054500D:C08
204	151	RTA22200019F.j.24.1.P.Seq	M00054520A:D04
205	151	RTA22200019F.k.01.1.P.Seq	M00054520A:D04
206	153	RTA22200019F.m.05.1.P.Seq	M00054538C:C01
207	154	RTA22200020F.i.12.1.P.Seq	M00054639D:F05
208	155	RTA22200020F.j.09.1.P.Seq	M00054647A:A09
209	156	RTA22200020F.j.24.1.P.Seq	M00054650D:E04
210	157	RTA22200021F.d.09.2.P.Seq	M00054742C:B12
211	158	RTA22200021F.g.18.3.P.Seq	M00054769A:E05
212	159	RTA22200021F.h.15.3.P.Seq	M00054777D:E09
213	160	RTA22200021F.i.23.3.P.Seq	M00054806B:G03
214	161	RTA22200022F.d.04.1.P.Seq	M00054893C:D03
215	162	RTA22200022F.m.09.1.P.Seq	M00054971D:D07
217	195	RTA22200024F.i.11.1.P.Seq	M00055209C:B07
218	164	RTA22200024F.p.03.1.P.Seq	M00055258B:D12
220	65	RTA22200026F.d.17.1.P.Seq	M00055423A:C07
222	124	RTA22200231F.b.20.1.P.Seq	M00007935D:A05
223	126	RTA22200231F.l.22.1.P.Seq	M00007985A:B08
224	132	RTA22200232F.d.23.1.P.Seq	M00021956B:A09
225	291	RTA22200232F.m.17.1.P.Seq	M00022140A:E11
226	142	RTA22200241F.e.15.1.P.Seq	M00026888A:A03
227	144	RTA22200241F.g.22.1.P.Seq	M00026903D:D11
228	115	X2.ga43_378506	M00003852B:C01
230	255	gb|AA024920.1|AA024920	RG:364972:10009:B06
231	262	gb|AA033519.1|AA033519	RG:471154:10009:H04

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
232	256	gb|AA039790.1|AA039790	RG:376554:10009:B12
233	263	gb|AA043829.1|AA043829	RG:487171:10009:H09
234	265	gb|AA070046.1|AA070046	RG:530002:10002:A08
235	264	gb|AA128438.1|AA128438	RG:526536:10002:A02
236	266	gb|AA179757.1|AA179757	RG:612874:10002:G02
239	269	gb|AA232253.1|AA232253	RG:666323:10010:B07
240	270	gb|AA234451.1|AA234451	RG:669110:10010:B12
242	273	gb|AA399596.1|AA399596	RG:729913:10010:G11
243	276	gb|AA400338.1|AA400338	RG:742764:10011:A06
247	236	gb|AA431134.1|AA431134	RG:781507:10011:E01
248	277	gb|AA446295.1|AA446295	RG:781028:10011:D08
249	278	gb|AA448898.1|AA448898	RG:785368:10011:E11
250	278	gb|AA449542.1|AA449542	RG:785846:10011:F02
252	274	gb|AA477696.1|AA477696	RG:740831:10010:H12
253	280	gb|AA530983.1|AA530983	RG:985973:10012:B09
254	259	gb|AA679027.1|AA679027	RG:432960:10009:E11
255	210	gb|AA723679.1|AA723679	RG:1325847:10012:H07
256	213	gb|AA829074.1|AA829074	RG:1374447:20004:G01
257	212	gb|AA830348.1|AA830348	RG:1353123:10013:A06
258	214	gb|AA885302.1|AA885302	RG:1461567:10013:E03
260	216	gb|AA926951.1|AA926951	RG:1552386:10013:G04
262	219	gb|AI004332.1|AI004332	RG:1631867:10014:B06
263	252	gb|AI015644.1|AI015644	RG:1635546:10014:B08
264	220	gb|AI017336.1|AI017336	RG:1638979:10014:C04
265	218	gb|AI018495.1|AI018495	RG:1630930:10014:B05
266	221	gb|AI031810.1|AI031810	RG:1645945:10014:D05
267	226	gb|AI054129.1|AI054129	RG:1861510:20001:B03
268	212	gb|AI066521.1|AI066521	RG:1637619:10014:C02
269	223	gb|AI076187.1|AI076187	RG:1674098:10014:H01
270	221	gb|AI079570.1|AI079570	RG:1674393:10014:H02
271	206	gb|AI123832.1|AI123832	RG:1651303:10014:E01
272	225	gb|AI207972.1|AI207972	RG:1838677:10015:E10
273	231	gb|AI224731.1|AI224731	RG:2002384:20003:E01
274	233	gb|AI265824.1|AI265824	RG:2006592:20003:F12
275	232	gb|AI279390.1|AI279390	RG:2006302:20003:F08
276	227	gb|AI298668.1|AI298668	RG:1895716:10015:G09
277	229	gb|AI305997.1|AI305997	RG:1996788:20003:C10
278	230	gb|AI306323.1|AI306323	RG:1996901:20003:D01
279	239	gb|AI335279.1|AI335279	RG:2055807:10016:B09
280	238	gb|AI336511.1|AI336511	RG:2051667:20003:H05
281	228	gb|AI347995.1|AI347995	RG:1927470:10015:H08
282	235	gb|AI356632.1|AI356632	RG:2012168:10016:B05

Table 2
Summary of Polynucleotides

SEQ ID NO	CID	Sequence Name	Sample Name or Clone Name
283	237	gb|AI375104.1|AI375104	RG:2048081:10016:B08
284	241	gb|AI421409.1|AI421409	RG:2097257:10016:C07
285	242	gb|AI421521.1|AI421521	RG:2097294:10016:C08
286	243	gb|AI523571.1|AI523571	RG:2117694:10016:E01
287	258	gb|H00135.1|H00135	RG:43296:10005:C03
288	261	gb|H08424.1|H08424	RG:45623:10005:D09
289	260	gb|H12948.1|H12948	RG:43534:10005:C04
290	236	gb|H54104.1|H54104	RG:203031:10007:A09
293	246	gb|N55598.1|N55598	RG:244601:10007:E02
294	245	gb|N75655.1|N75655	RG:244132:10007:E01
295	248	gb|N98702.1|N98702	RG:278409:10008:B10
296	129	gb|R12138.1|R12138	RG:25258:10004:D09
298	2	gb|R17980.1|R17980	RG:32281:10004:G05
299	254	gb|R21293.1|R21293	RG:35892:10004:H10
300	249	gb|R41558.1|R41558	RG:29739:10004:F02
301	2	gb|R56713.1|R56713	RG:41097:10005:B10
302	224	gb|R85309.1|R85309	RG:180296:10006:G03
303	222	gb|R87679.1|R87679	RG:166410:10006:F01
304	208	gb|T83145.1|T83145	RG:110764:10005:H04
305	250	gb|W16960.1|W16960	RG:301608:10008:D09
306	251	gb|W24201.1|W24201	RG:306813:10008:E12
307	252	gb|W45587.1|W45587	RG:323425:10008:F11
308	253	gb|W69496.1|W69496	RG:343821:10008:H05
309	257	gb|W87460.1|W87460	RG:417109:10009:D09

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
1	114	D29958	gi|473948|dbj|D29958.1|HUMORFA10 Human mRNA for KIAA0116 gene, partial cds	573	1011	1E-162	289/289
2	123	NM_020510	gi|10048405|ref|NM_020510.1| Mus musculus frizzled homolog 10 (Drosophila) (Fzd10), mRNA	77.8	2112	3E-12	39/39
3	114	D29958	gi|473948|dbj|D29958.1|HUMORFA10 Human mRNA for KIAA0116 gene, partial cds	969	1011	0	559/575
4	1	XM_001344	gi|11421753|ref|XM_001344.1| Homo sapiens S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), mRNA	464	512	1E-129	234/234
5	2	NM_004443	gi|4758287|ref|NM_004443.1| Homo sapiens EphB3 (EPHB3) mRNA	194	3805	3E-48	137/145
6	3	BC001014	gi|12654380|gb|BC001014.1|BC001014 Homo sapiens, Similar to methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase, clone IMAGE:3344724, mRNA, partial cds	444	1378	1E-123	224/224
7	4	NM_001363	gi|4503336|ref|NM_001363.1| Homo sapiens dyskeratosis congenita 1, dyskerin (DKC1), mRNA	513	2422	1E-144	259/259
8	5	NM_001699	gi|11863124|ref|NM_001699.2| Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 2, mRNA	543	4986	1E-153	281/282
9	6	NM_001827	gi|4502858|ref|NM_001827.1| Homo sapiens CDC28 protein kinase 2 (CKS2), mRNA	535	627	1E-150	279/282
10	7	XM_011126	gi|12730374|ref|XM_011126.1| Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), mRNA	515	2219	1E-144	260/260
11	8	BC002718	gi|12803760|gb|BC002718.1|BC002718 Homo sapiens, type I transmembrane protein Fn14, clone MGC:3386, mRNA, complete cds	299	1028	1E-79	223/236

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
12	9	XM_007891	gi|11430799|ref|XM_007891.1| Homo sapiens cadherin 3, type 1, P-cadherin (placental) (CDH3), mRNA	317	3171	3E-85	160/160
13	10	BC001883	gi|12804870|gb|BC001883.1|BC001883 Homo sapiens, nucleolar phosphoprotein p130, clone MGC:1494, mRNA, complete cds	490	2464	1E-137	255/259
14	11	XM_002532	gi|11429973|ref|XM_002532.1| Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA	440	1132	1E-122	244/255
15	12	BC005334	gi|13529121|gb|BC005334.1|BC005334 Homo sapiens, centrin, EF-hand protein, 2, clone MGC:12421, mRNA, complete cds	494	1047	1E-138	258/260
16	13	XM_009001	gi|12742166|ref|XM_009001.2| Homo sapiens kallikrein 6 (neurosin, zyme) (KLK6), mRNA	462	1506	1E-128	233/233
17	14	XM_005818	gi|12735488|ref|XM_005818.2| Homo sapiens arachidonate 5-lipoxygenase (ALOX5), mRNA	373	2420	1E-102	188/188
18	15	XM_012273	gi|12737900|ref|XM_012273.1| Homo sapiens forkhead box M1 (FOXM1), mRNA	396	3314	1E-109	200/200
19	167	AK000140	gi|7020034|dbj|AK000140.1|AK000140 Homo sapiens cDNA FLJ20133 fis, clone COL06539	1114	1403	0	587/596
20	16	BC003146	gi|13111946|gb|BC003146.1|BC003146 Homo sapiens, splicing factor 3b, subunit 3, 130kD, clone MGC:3924, mRNA, complete cds	432	1720	1E-119	218/218

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
21	17	BC001763	gi|12804676|gb|BC001763.1|BC001763 Homo sapiens, Similar to translocase of outer mitochondrial membrane 34, clone MGC:1252, mRNA, complete cds	404	1917	1E-111	206/207
22	18	XM_007326	gi|11434291|ref|XM_007326.1| Homo sapiens bone morphogenetic protein 4 (BMP4), mRNA	404	1944	1E-111	204/204
23	19	XM_005376	gi|12734932|ref|XM_005376.2| Homo sapiens Friedreich ataxia (FRDA), mRNA	371	1503	1E-101	192/194
24	20	XM_010945	gi|12729201|ref|XM_010945.1| Homo sapiens hypothetical gene supported by XM_010945 (LOC65371), mRNA	452	614	1E-125	228/228
25	21	AK018953	gi|12858931|dbj|AK018953.1|AK018953 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700111D04, full insert sequence	174	1297	5E-42	174/203
26	22	BC003635	gi|13177711|gb|BC003635.1|BC003635 Homo sapiens, matrix metalloproteinase 7 (matrilysin, uterine), clone MGC:3913, mRNA, complete cds	456	1140	1E-127	230/230
27	23	XM_008589	gi|11427373|ref|XM_008589.1| Homo sapiens pyrroline-5-carboxylate reductase 1 (PYCR1), mRNA	440	1790	1E-122	224/225
28	24	BC001880	gi|12804864|gb|BC001880.1|BC001880 Homo sapiens, Similar to insulin induced gene 1, clone MGC:1405, mRNA, complete cds	379	1469	1E-103	191/191
29	25	XM_003047	gi|12729625|ref|XM_003047.2| Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin) (MCM2), mRNA	353	3383	7E-96	178/178
30	26	NC_002548	gi|10314009|ref|NC_002548.1| Acute bee paralysis virus, complete genome	38.2	9491	0.68	19/19
31	170	NM_004219	gi|11038651|ref|NM_004219.2| Homo sapiens pituitary tumor-transforming 1 (PTTG1), mRNA	1314	728	0	667/669
32	27	BC002479	gi|12803322|gb|BC002479.1|BC002479 Homo sapiens, cathepsin H, clone MGC:1519, mRNA, complete cds	613	1479	1E-174	309/309
33	28	BC000123	gi|12652744|gb|BC000123.1|BC000123 Homo sapiens, pyridoxal (pyridoxine, vitamin B6) kinase, clone MGC:3128, mRNA, complete cds	545	1331	1E-153	275/275

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
34	29	AK000836	gi|7021154|dbj|AK000836.1|AK000836 Homo sapiens cDNA FLJ20829 fis, clone ADKA03163, highly similar to D26488 Human mRNA for KIAA0007 gene	406	1703	1E-112	205/205
35	30	BC001425	gi|12655140|gb|BC001425.1|BC001425 Homo sapiens, Similar to differential display and activated by p53, clone MGC:1780, mRNA, complete cds	504	2499	1E-141	256/257
36	31	BC005301	gi|13529028|gb|BC005301.1|BC005301 Homo sapiens, integrin beta 3 binding protein (beta3-endonexin), clone MGC:12370, mRNA, complete cds	442	998	1E-122	225/226
37	32	Z27409	gi|482916|emb|Z27409.1|HSRTKEPH H.sapiens mRNA for receptor tyrosine kinase eph (partial)	529	2398	1E-149	276/278
38	33	XM_003107	gi|12729732|ref|XM_003107.2| Homo sapiens transketolase (Wernicke-Korsakoff syndrome) (TKT), mRNA	436	1985	1E-120	227/228
39	34	AB002297	gi|2224538|dbj|AB002297.1|AB002297 Human mRNA for KIAA0299 gene, partial cds	387	8063	1E-106	208/211
40	35	XM_002591	gi|12728749|ref|XM_002591.2| Homo sapiens KIAA0173 gene product (KIAA0173), mRNA	502	4732	1E-140	253/253
41	36	XM_009101	gi|11425196|ref|XM_009101.1| Homo sapiens fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) (FUT1), mRNA	523	3374	1E-147	271/272
42	37	AF082858	gi|4587463|gb|AF082858.1|AF082858 Homo sapiens pterin carbinolamine dehydratase (PCD) mRNA, complete cds	494	829	1E-138	249/249
43	38	BC001600	gi|12804396|gb|BC001600.1|BC001600 Homo sapiens, D123 gene product, clone MGC:1935, mRNA, complete cds	533	1316	1E-150	269/269
44	39	BC000871	gi|12654114|gb|BC000871.1|BC000871 Homo sapiens, annexin A3, clone MGC:5043, mRNA, complete cds	609	1489	1E-172	307/307
45	41	AL136600	gi|13276700|emb|AL136600.1|HSM801574 Homo sapiens mRNA; cDNA DKFZp564I1216 (from clone DKFZp564I1216); complete cds	504	1552	1E-141	254/254

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
46	42	AK024772	gi|10437149|dbj|AK024772.1|AK024772 Homo sapiens cDNA: FLJ21119 fis, clone CAS05644, highly similar to HSA272196 Homo sapiens mRNA for hypothetical protein	484	864	1E-135	246/247
47	43	BC004246	gi|13279007|gb|BC004246.1|BC004246 Homo sapiens, mutS (E. coli) homolog 6, clone MGC:10498, mRNA, complete cds	438	4249	1E-121	221/221
48	44	X92474	gi|1045056|emb|X92474.1|HSCHTOG H.sapiens mRNA for ch-TOG protein	238	6449	2E-61	122/123
49	45	BC002994	gi|12804270|gb|BC002994.1|BC002994 Homo sapiens, clone MGC:3823, mRNA, complete cds	476	2238	1E-132	246/248
50	46	AK025062	gi|10437501|dbj|AK025062.1|AK025062 Homo sapiens cDNA: FLJ21409 fis, clone COL03924	327	2692	4E-88	174/176
51	47	AP001247	gi|10121151|dbj|AP001247.3|AP001247 Homo sapiens genomic DNA, chromosome 2p11.2, clone:lambda316	36.2	16950	2.8	20/21
52	48	AF131838	gi|4406677|gb|AF131838.1|AF131838 Homo sapiens clone 25107 mRNA sequence	498	1462	1E-139	251/251
53	49	XM_007647	gi|11432476|ref|XM_007647.1| Homo sapiens immunoglobulin superfamily containing leucine-rich repeat (ISLR), mRNA	531	2111	1E-149	268/268
54	50	AB048286	gi|13537296|dbj|AB048286.1|AB048286 Homo sapiens GS1999full mRNA, complete cds	476	2713	1E-132	247/248
56	53	AK001515	gi|7022818|dbj|AK001515.1|AK001515 Homo sapiens cDNA FLJ10653 fis, clone NT2RP2005890	333	884	6E-90	168/168
57	54	AB023156	gi|4589521|dbj|AB023156.1|AB023156 Homo sapiens mRNA for KIAA0939 protein, partial cds	42.1	5537	0.055	24/25
58	55	XM_008622	gi|12740774|ref|XM_008622.2| Homo sapiens thymidine kinase 1, soluble (TK1), mRNA	507	1427	1E-142	256/256
59	56	XM_003758	gi|11416585|ref|XM_003758.1| Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA	422	2691	1E-116	215/216
60	58	XM_001732	gi|11423748|ref|XM_001732.1| Homo sapiens calcyclin binding protein (CACYBP), mRNA	500	2435	1E-140	252/252

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Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
61	59	BC001866	gi|12804840|gb|BC001866.1|BC001866 Homo sapiens, replication factor C (activator 1) 5 (36.5kD), clone MGC:1155, mRNA, complete cds	396	2097	1E-109	239/256
62	60	BC000293	gi|12653056|gb|BC000293.1|BC000293 Homo sapiens, non-metastatic cells 1, protein (NM23A) expressed in, clone MGC:8334, mRNA, complete cds	87.7	733	2E-16	58/65
63	63	XM_008043	gi|12739769|ref|XM_008043.2| Homo sapiens dipeptidase 1 (renal) (DPEP1), mRNA	519	1739	1E-146	262/262
64	64	AB052751	gi|11967903|dbj|AB052751.1|AB052751 Homo sapiens Axin2 mRNA for conductin, partial cds and 3'UTR	527	1863	1E-148	266/266
65	65	BC005832	gi|13543336|gb|BC005832.1|BC005832 Homo sapiens, KIAA0101 gene product, clone MGC:2250, mRNA, complete cds	460	1444	1E-128	232/232
66	66	XM_002190	gi|11428365|ref|XM_002190.1| Homo sapiens chromosome 1 open reading frame 2 (C1ORF2), mRNA	472	3152	1E-131	238/238
67	67	XM_010360	gi|12743462|ref|XM_010360.2| Homo sapiens transcription factor NRF (NRF), mRNA	505	3746	1E-141	255/255
68	68	AL122064	gi|6102857|emb|AL122064.1|HSM801208 Homo sapiens mRNA; cDNA DKFZp434M231 (from clone DKFZp434M231); partial cds	502	1320	1E-140	257/259
70	71	XM_005226	gi|11425871|ref|XM_005226.1| Homo sapiens antizyme inhibitor (LOC51582), mRNA	507	2619	1E-142	256/256
71	74	BC002956	gi|12804196|gb|BC002956.1|BC002956 Homo sapiens, ClpP (caseinolytic protease, ATP-dependent, proteolytic subunit, E. coli) homolog, clone MGC:1379, mRNA, complete cds	484	1185	1E-135	244/244
73	100	NM_014791	gi|7661973|ref|NM_014791.1| Homo sapiens KIAA0175 gene product (KIAA0175), mRNA	1211	2470	0	691/708
74	105	BC005864	gi|13543414|gb|BC005864.1|BC005864 Homo sapiens, cyclin-dependent kinase 4, clone MGC:3719, mRNA, complete cds	1108	1430	0	621/635
75	106	XM_005404	gi|11428250|ref|XM_005404.1| Homo sapiens catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA	1203	2446	0	631/638

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Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
76	104	BC002362	gi|12803116|gb|BC002362.1|BC002362 Homo sapiens, lactate dehydrogenase B, clone MGC:8627, mRNA, complete cds	1269	1318	0	643/644
77	75	AF065389	gi|3152702|gb|AF065389.1|AF065389 Homo sapiens tetraspan NET-4 mRNA, complete cds	434	1405	1E-120	236/244
78	76	BC004863	gi|13436073|gb|BC004863.1|BC004863 Homo sapiens, Similar to phosphoserine aminotransferase, clone MGC:10519, mRNA, complete cds	587	2229	1E-166	303/304
79	77	XM_011917	gi|12735709|ref|XM_011917.1| Homo sapiens adenosine kinase (ADK), mRNA	509	1414	1E-143	259/260
80	78	BC000897	gi|12654158|gb|BC000897.1|BC000897 Homo sapiens, interferon induced transmembrane protein 1 (9-27), clone MGC:5195, mRNA, complete cds	143	683	8E-33	102/107
81	79	NM_014641	gi|7661965|ref|NM_014641.1| Homo sapiens KIAA0170 gene product (KIAA0170), mRNA	335	6940	3E-90	196/206
82	80	XM_012967	gi|12742527|ref|XM_012967.1| Homo sapiens RAE1 (RNA export 1, S.pombe) homolog (RAE1), mRNA	430	1188	1E-119	231/233
83	81	XM_003913	gi|12719136|ref|XM_003913.2| Homo sapiens integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2), mRNA	571	5348	1E-161	288/288
84	109	AK024039	gi|10436304|dbj|AK024039.1|AK024039 Homo sapiens cDNA FLJ13977 fis, clone Y79AA1001603, weakly similar to POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)	422	2224	1E-116	377/443
85	110	XM_009492	gi|11420665|ref|XM_009492.1| Homo sapiens v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2), mRNA	852	2627	0	440/444
86	111	XM_009587	gi|12742401|ref|XM_009587.2| Homo sapiens TH1 drosophila homolog (HSPC130), mRNA	749	2108	0	392/394
87	121	NM_001408	gi|13325063|ref|NM_001408.1| Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog (CELSR2), mRNA	1067	10531	0	627/660

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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
88	118	AF226998	gi|12655885|gb|AF226998.1|AF226998 Homo sapiens dpy-30-like protein mRNA, complete cds	775	734	0	391/391
89	41	BC001106	gi|12654544|gb|BC001106.1|BC001106 Homo sapiens, hypothetical protein, clone MGC:891, mRNA, complete cds	416	1542	1E-114	214/216
90	139	XM_009005	gi|11424670|ref|XM_009005.1| Homo sapiens kallikrein 11 (KLK11), mRNA	1112	1186	0	617/630
91	83	XM_006067	gi|12736004|ref|XM_006067.2| Homo sapiens 7-dehydrocholesterol reductase (DHCR7), mRNA	321	2525	4E-86	189/194
92	85	AF092569	gi|3986473|gb|AF092569.1|HSEIFP1 Homo sapiens translation initiation factor eIF3 p40 subunit gene, exon 1	87.7	299	2E-16	74/79
93	117	BC004264	gi|13279061|gb|BC004264.1|BC004264 Homo sapiens, Similar to EphB4, clone IMAGE:3611312, mRNA, partial cds	1021	3138	0	564/582
94	113	BC000277	gi|12802987|gb|BC000277.1|BC000277 Homo sapiens, clone MGC:1892, mRNA, complete cds	1011	2947	0	586/618
95	87	NM_015339	gi|12229216|ref|NM_015339.1| Homo sapiens activity-dependent neuroprotective protein (ADNP), mRNA	599	4713	1E-169	302/302
96	88	XM_009845	gi|11526339|ref|XM_009845.1| Homo sapiens catechol-O-methyltransferase (COMT), mRNA	505	1291	1E-141	255/255
97	89	BC000509	gi|12653474|gb|BC000509.1|BC000509 Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 7, clone MGC:8507, mRNA, complete cds	517	1008	1E-145	261/261
98	125	AK024618	gi|10436934|dbj|AK024618.1|AK024618 Homo sapiens cDNA: FLJ20965 fis, clone ADSH01104	1199	1804	0	662/676
99	128	D80001	gi|1136417|dbj|D80001.1|D80001 Human mRNA for KIAA0179 gene, partial cds	1138	4994	0	639/663
100	127	BC004899	gi|13436169|gb|BC004899.1|BC004899 Homo sapiens, sigma receptor (SR31747 binding protein 1), clone MGC:3851, mRNA, complete cds	930	1688	0	579/619
101	129	BC003129	gi|13111916|gb|BC003129.1|BC003129 Homo sapiens, non-POU-domain-containing, octamer-binding, clone MGC:3380, mRNA, complete cds	1043	1882	0	583/602

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Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
102	130	XM_009690	gi|12742251|ref|XM_009690.2| Homo sapiens hypothetical protein FLJ10850 (FLJ10850), mRNA	438	2277	1E-121	367/404
104	136	XM_005908	gi|11432093|ref|XM_005908.1| Homo sapiens hypothetical protein FLJ10540 (FLJ10540), mRNA	1235	2237	0	642/646
106	5	NM_001699	gi|11863124|ref|NM_001699.2| Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 2, mRNA	922	4986	0	550/572
107	137	NM_025927	gi|13385417|ref|NM_025927.1| Mus musculus RIKEN cDNA 2600005P05 gene (2600005P05Rik), mRNA	228	1486	1E-57	223/259
108	138	AK023154	gi|10434948|dbj|AK023154.1|AK023154 Homo sapiens cDNA FLJ13092 fis, clone NT2RP3002147	924	3040	0	524/541
109	141	AB017710	gi|5821114|dbj|AB017710.1|AB017710 Homo sapiens U50HG genes for U50' snoRNA and U50 snoRNA, complete sequence	1067	2353	0	570/582
110	90	NM_011775	gi|6756080|ref|NM_011775.1| Mus musculus zona pellucida glycoprotein 2 (Zp2), mRNA	40.1	2185	0.21	20/20
111	145	AF086315	gi|3483660|gb|AF086315.1|HUMZD52F10 Homo sapiens full length insert cDNA clone ZD52F10	841	600	0	467/480
112	91	XM_002596	gi|12728741|ref|XM_002596.2| Homo sapiens protein tyrosine phosphatase, receptor type, N (PTPRN), mRNA	361	2877	4E-98	201/209
113	92	XM_004484	gi|11418942|ref|XM_004484.1| Homo sapiens tumor protein D52-like 1 (TPD52L1), mRNA	482	1325	1E-134	243/243
114	93	BC000331	gi|12653128|gb|BC000331.1|BC000331 Homo sapiens, proteasome (prosome, macropain) subunit, beta type, 4, clone MGC:8522, mRNA, complete cds	583	935	1E-165	305/310
116	100	NM_014791	gi|7661973|ref|NM_014791.1| Homo sapiens KIAA0175 gene product (KIAA0175), mRNA	1185	2470	0	644/664
118	123	XM_004185	gi|12731991|ref|XM_004185.2| Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA	751	4092	0	463/481
119	94	XM_004750	gi|12733059|ref|XM_004750.2| Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1), mRNA	484	629	1E-135	244/244
120	95	XM_006928	gi|12737727|ref|XM_006928.2| Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA	412	4870	1E-113	239/248

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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
121	96	AL133104	gi|6453587|emb|AL133104.1|HSM801384 Homo sapiens mRNA; cDNA DKFZp434E1822 (from clone DKFZp434E1822); partial cds	601	1186	1E-170	303/303
122	98	BC004528	gi|13528647|gb|BC004528.1|BC004528 Homo sapiens, clone MGC:3017, mRNA, complete cds	466	2751	1E-129	244/246
123	103	AF097514	gi|4808600|gb|AF097514.1|AF097514 Homo sapiens stearoyl-CoA desaturase (SCD) mRNA, complete cds	1302	5221	0	721/738
124	103	AF097514	gi|4808600|gb|AF097514.1|AF097514 Homo sapiens stearoyl-CoA desaturase (SCD) mRNA, complete cds	1328	5221	0	720/734
125	133	AF220656	gi|7107358|gb|AF220656.1|AF220656 Homo sapiens apoptosis-associated nuclear protein PHLDA1 (PHLDA1) mRNA, partial cds	936	3227	0	529/539
126	133	AF220656	gi|7107358|gb|AF220656.1|AF220656 Homo sapiens apoptosis-associated nuclear protein PHLDA1 (PHLDA1) mRNA, partial cds	969	3227	0	544/555
130	115	AF019770	gi|2674084|gb|AF019770.1|AF019770 Homo sapiens macrophage inhibitory cytokine-1 (MIC-1) mRNA, complete cds	1277	1202	0	735/751
131	106	AK022926	gi|10434597|dbj|AK022926.1|AK022926 Homo sapiens cDNA FLJ12864 fis, clone NT2RP2003604, highly similar to Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA	589	2455	1E-166	299/300
132	113	BC000277	gi|12802987|gb|BC000277.1|BC000277 Homo sapiens, clone MGC:1892, mRNA, complete cds	513	2947	1E-144	262/263
133	113	XM_006213	gi|12736410|ref|XM_006213.2| Homo sapiens KIAA0712 gene product (KIAA0712), mRNA	579	6477	1E-163	299/300
134	106	XM_005404	gi|11428250|ref|XM_005404.1| Homo sapiens catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA	561	2446	1E-158	300/306
135	116	BC001068	gi|12654476|gb|BC001068.1|BC001068 Homo sapiens, clone IMAGE:2823731, mRNA, partial cds	595	2333	1E-168	300/300
136	117	BC004264	gi|13279061|gb|BC004264.1|BC004264 Homo sapiens, Similar to EphB4, clone IMAGE:3611312, mRNA, partial cds	486	3138	1E-135	250/252

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
138	123	Y09668	gi|1834428|emb|Y09668.1|DRTKLELF1 D.rerio mRNA for tyrosine kinase ligand (elf-1)	36.2	2272	3.5	18/18
140	140	XM_008802	gi|12741169|ref|XM_008802.2| Homo sapiens retinoblastoma-binding protein 8 (RBBP8), mRNA	710	3185	0	358/358
141	143	XM_009111	gi|12741675|ref|XM_009111.2| Homo sapiens sulfotransferase family, cytosolic, 2B, member 1 (SULT2B1), mRNA	672	1453	0	362/367
142	121	NM_001408	gi|13325063|ref|NM_001408.1| Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog (CELSR2), mRNA	755	10531	0	388/389
143	121	NM_001408	gi|13325063|ref|NM_001408.1| Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog (CELSR2), mRNA	741	10531	0	376/377
144	139	XM_009005	gi|11424670|ref|XM_009005.1| Homo sapiens kallikrein 11 (KLK11), mRNA	622	1186	1E-176	340/346
145	112	XM_003733	gi|12731080|ref|XM_003733.2| Homo sapiens DEAD-box protein abstrakt (ABS), mRNA	753	2088	0	380/380
147	166	AF216754	gi|6707650|gb|AF216754.1|AF216754 Homo sapiens over-expressed breast tumor protein (OBTP) mRNA, complete cds	567	354	1E-160	296/298
148	167	XM_003384	gi|12730453|ref|XM_003384.2| Homo sapiens hypothetical protein (LOC51316), mRNA	640	748	0	323/323
149	169	XM_009527	gi|11420875|ref|XM_009527.1| Homo sapiens secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI), mRNA	751	594	0	382/383
150	30	AF279897	gi|12751120|gb|AF279897.1|AF279897 Homo sapiens PNAS-143 mRNA, complete cds	654	727	0	333/334
151	170	NM_004219	gi|11038651|ref|NM_004219.2| Homo sapiens pituitary tumor-transforming 1 (PTTG1), mRNA	730	728	0	368/368
152	171	S76771	gi|914225|gb|S76771.1|S76771 TPO=thrombopoietin [human, Genomic, 6849 nt]	210	6849	1E-52	168/185
153	171	M81890	gi|186274|gb|M81890.1|HUMIL11A Human interleukin 11 (IL11) gene, complete mRNA	216	6870	2E-54	180/203

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
154	172	XM_004952	gi|12733392|ref|XM_004952.2| Homo sapiens solute carrier family 26, member 3 (SLC26A3), mRNA	603	2861	1E-171	310/312
155	147	XM_009488	gi|12742285|ref|XM_009488.2| Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA	716	770	0	361/361
156	149	XM_011755	gi|12734624|ref|XM_011755.1| Homo sapiens SET translocation (myeloid leukemia-associated) (SET), mRNA	733	2566	0	370/370
157	150	L19183	gi|307154|gb|L19183.1|HUMMAC30X Human MAC30 mRNA, 3' end	593	2002	1E-168	323/331
158	151	AK024303	gi|10436651|dbj|AK024303.1|AK024303 Homo sapiens cDNA FLJ14241 fis, clone OVARC1000533	698	1591	0	352/352
159	173	BC001410	gi|12655116|gb|BC001410.1|BC001410 Homo sapiens, S100 calcium-binding protein A11 (calgizzarin), clone MGC:2149, mRNA, complete cds	682	577	0	354/356
161	175	BC001308	gi|12654922|gb|BC001308.1|BC001308 Homo sapiens, clone HQ0310 PRO0310p1, clone MGC:5505, mRNA, complete cds	646	2263	0	353/362
162	176	XM_009004	gi|12742171|ref|XM_009004.2| Homo sapiens kallikrein 10 (KLK10), mRNA	458	1448	1E-127	231/231
163	177	XM_006705	gi|12737366|ref|XM_006705.2| Homo sapiens nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA	630	784	1E-179	324/326
164	178	AF102848	gi|12641918|gb|AF102848.1|AF102848 Homo sapiens keratin 23 (KRT23) mRNA, complete cds	739	1649	0	379/381
165	179	XM_003512	gi|12730699|ref|XM_003512.2| Homo sapiens amphiregulin (schwannoma-derived growth factor) (AREG), mRNA	718	1231	0	371/374
166	180	XM_005313	gi|12734542|ref|XM_005313.2| Homo sapiens gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) (GGH), mRNA	652	1275	0	335/337
168	182	XM_010117	gi|11419764|ref|XM_010117.1| Homo sapiens plastin 3 (T isoform) (PLS3), mRNA	690	2519	0	360/364
169	183	L47277	gi|986911|gb|L47277.1|HUMTOPATRA Homo sapiens (cell line HepG2, HeLa) alpha topoisomerase truncated-form mRNA, 3'UTR	646	994	0	353/362

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
170	184	XM_012941	gi|12742342|ref|XM_012941.1| Homo sapiens chromosome 20 open reading frame 1 (C20ORF1), mRNA	670	3071	0	341/342
171	185	NM_000581	gi|10834975|ref|NM_000581.1| Homo sapiens glutathione peroxidase 1 (GPX1), mRNA	640	1134	0	339/343
172	185	NM_000581	gi|10834975|ref|NM_000581.1| Homo sapiens glutathione peroxidase 1 (GPX1), mRNA	640	1134	0	338/343
173	186	X06705	gi|35511|emb|X06705.1|HSPLAX Human PLA-X mRNA	700	883	0	353/353
174	187	D45915	gi|1483130|dbj|D45915.1|D45915 Human mRNA for p80 protein, complete cds	666	2584	0	336/336
176	189	BC000242	gi|12652962|gb|BC000242.1|BC000242 Homo sapiens, CGI 138 protein, clone MGC:676, mRNA, complete cds	521	849	1E-146	280/286
177	190	BC005945	gi|13543585|gb|BC005945.1|BC005945 Homo sapiens, MAD2 (mitotic arrest deficient, yeast, homolog)-like 1, clone MGC:14577, mRNA, complete cds	567	1391	1E-160	295/298
179	192	XM_010835	gi|12728550|ref|XM_010835.1| Homo sapiens similar to hypothetical protein (H. sapiens) (LOC65349), mRNA	452	1679	1E-125	313/340
180	193	XM_009475	gi|11420562|ref|XM_009475.1| Homo sapiens S-adenosylhomocysteine hydrolase (AHCY), mRNA	668	2110	0	340/341
181	194	AF054183	gi|4092053|gb|AF054183.1|AF054183 Homo sapiens GTP binding protein mRNA, complete cds	690	1148	0	351/352
182	195	BC005356	gi|13529175|gb|BC005356.1|BC005356 Homo sapiens, Similar to hypothetical protein MGC3077, clone MGC:12457, mRNA, complete cds	396	1050	1E-108	200/200
183	196	XM_006545	gi|12736918|ref|XM_006545.2| Homo sapiens hypothetical protein (HSPC152), mRNA	613	588	1E-173	309/309
184	197	XM_003598	gi|12730828|ref|XM_003598.2| Homo sapiens S100 calcium binding protein P (S100P), mRNA	662	440	0	345/349
185	197	NM_005980	gi|5174662|ref|NM_005980.1| Homo sapiens S100 calcium-binding protein P (S100P), mRNA	565	439	1E-159	291/293
190	199	M80340	gi|339767|gb|M80340.1|HUMTNL12 Human transposon L1.1 with a base deletion relative to L1.2B resulting in a premature stop codon in the coding region	539	6075	1E-151	351/377

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
191	199	U93574	gi|2072975|gb|U93574.1|HSU93574 Human L1 element L1.39 p40 and putative p150 genes, complete cds	404	5979	1E-111	290/318
192	200	AC002143	gi|2168303|gb|AC002143.1|AC002143 Homo sapiens (subclone 4_b10 from BAC H102) DNA sequence, complete sequence	214	4025	8E-54	235/275
193	176	BC002710	gi|12803744|gb|BC002710.1|BC002710 Homo sapiens, kallikrein 10, clone MGC:3667, mRNA, complete cds	648	1542	0	327/327
194	201	XM_004286	gi|11418526|ref|XM_004286.1| Homo sapiens ribosomal protein L10a (RPL10A), mRNA	561	700	1E-158	289/291
196	118	AF226998	gi|12655885|gb|AF226998.1|AF226998 Homo sapiens dpy-30-like protein mRNA, complete cds	505	734	1E-141	255/255
198	204	AL3900221	gi|10862787|emb|AL390022.11|AL390022 Human DNA sequence from clone RP11-370B6 on chromosome X, complete sequence [Homo sapiens]	470	9277	1E-130	337/369
200	206	BC002476	gi|12803316|gb|BC002476.1|BC002476 Homo sapiens, non-metastatic cells 2, protein (NM23B) expressed in, clone MGC:2212, mRNA, complete cds	615	695	1E-174	316/318
201	207	XM_005235	gi|12734360|ref|XM_005235.2| Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6), mRNA	605	1507	1E-171	311/313
202	152	BC004427	gi|13325215|gb|BC004427.1|BC004427 Homo sapiens, proteasome (prosome, macropain) subunit, alpha type, 7, clone MGC:3755, mRNA, complete cds	611	967	1E-173	321/324
204	151	AK024303	gi|10436651|dbj|AK024303.1|AK024303 Homo sapiens cDNA FLJ14241 fis, clone OVARC1000533	585	1591	1E-165	295/295
205	151	AK024303	gi|10436651|dbj|AK024303.1|AK024303 Homo sapiens cDNA FLJ14241 fis, clone OVARC1000533	591	1591	1E-167	298/298
206	153	XM_003927	gi|11417090|ref|XM_003927.1| Homo sapiens Apg12 (autophagy 12, S. cerevisiae)-like (APG12L), mRNA	656	473	0	337/339
207	154	BC000947	gi|13111828|gb|BC000947.2|BC000947 Homo sapiens, clone IMAGE:3450586, mRNA, partial cds	644	1608	0	336/340
208	155	XM_004478	gi|12732587|ref|XM_004478.2| Homo sapiens glyoxalase I (GLO1), mRNA	660	1993	0	339/341

Table 3
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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
209	156	L36587	gi|598241|gb|L36587.1|HUMUHGA Homo sapiens spliced UHG RNA	664	1357	0	335/335
210	157	BC000447	gi|12653354|gb|BC000447.1|BC000447 Homo sapiens, macrophage migration inhibitory factor (glycosylation-inhibiting factor), clone MGC:8444, mRNA, complete cds	656	585	0	334/335
211	158	BC001708	gi|12804576|gb|BC001708.1|BC001708 Homo sapiens, ribosomal protein S3A, clone MGC:1626, mRNA, complete cds	626	906	1E-178	319/320
212	159	BC005008	gi|13477106|gb|BC005008.1|BC005008 Homo sapiens, carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen), clone MGC:10467, mRNA, complete cds	668	2249	0	337/337
213	160	AL110141	gi|5817036|emb|AL110141.1|HSM800785 Homo sapiens mRNA; cDNA DKFZp564D0164 (from clone DKFZp564D0164)	519	656	1E-145	265/266
214	161	NM_014366	gi|7657047|ref|NM_014366.1| Homo sapiens putative nucleotide binding protein, estradiol-induced (E2IG3), mRNA	634	2059	1E-180	335/343
215	162	AL359585	gi|8655645|emb|AL359585.1|HSM802687 Homo sapiens mRNA; cDNA DKFZp762B195 (from clone DKFZp762B195)	129	2183	4E-28	68/69
217	195	NM_024051	gi|13129017|ref|NM_024051.1| Homo sapiens hypothetical protein MGC3077 (MGC3077), mRNA	646	1195	0	329/330
218	164	XM_006551	gi|11441541|ref|XM_006551.1| Homo sapiens interferon induced transmembrane protein 2 (1-8D) (IFITM2), mRNA	601	905	1E-170	321/327
220	65	XM_007736	gi|11433251|ref|XM_007736.1| Homo sapiens KIAA0101 gene product (KIAA0101), mRNA	648	836	0	330/331
222	124	U07571	gi|497170|gb|U07571.1|HSU07571 Human clone S1X13-SS13A dinucleotide repeat at Xq21	46.1	392	0.005	23/23
223	126	AF288394	gi|12620197|gb|AF288394.1|AF288394 Homo sapiens C1orf19 mRNA, partial cds	718	1961	0	377/382

Table 3
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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
224	132	U35622	gi|5733846|gb|U35622.2|HSU35622 Homo sapiens EWS protein/E1A enhancer binding protein chimera mRNA, complete cds	779	2107	0	398/400
225	291	BC004928	gi|13436256|gb|BC004928.1|BC004928 Homo sapiens, clone MGC:10493, mRNA, complete cds	793	2567	0	400/400
226	142	AL137736	gi|6808315|emb|AL137736.1|HSM802318 Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321)	692	2053	0	363/365
227	144	XM_008130	gi|11424226|ref|XM_008130.1| Homo sapiens galactokinase 1 (GALK1), mRNA	785	1361	0	396/396
228	115	AF019770	gi|2674084|gb|AF019770.1|AF019770 Homo sapiens macrophage inhibitory cytokine-1 (MIC-1) mRNA, complete cds	1370	1202	0	721/729
230	255	AF179710	gi|9836821|gb|AF179710.1|AF179710 Pongo pygmaeus RH50 glycoprotein (RHAG) gene, intron 9	40.1	1096	0.35	20/20
231	262	XM_009943	gi|11418022|ref|XM_009943.1| Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA	864	5486	0	455/462
232	256	AF134904	gi|4809150|gb|AF134904.1|AF134904 Schistocerca gregaria semaphorin 2a mRNA, complete cds	42.1	2558	0.097	21/21
233	263	BC003002	gi|12804286|gb|BC003002.1|BC003002 Homo sapiens, polo (Drosophia)-like kinase, clone MGC:3988, mRNA, complete cds	523	2165	1E-147	284/294
234	265	M68513	gi|199119|gb|M68513.1|MUSMEK4 Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds	882	3197	0	491/503
235	264	XM_007931	gi|12739533|ref|XM_007931.2| Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2 (SLC9A3R2), mRNA	730	1593	0	407/414
236	266	XM_003748	gi|12731108|ref|XM_003748.2| Homo sapiens serum-inducible kinase (SNK), mRNA	387	2967	1E-106	267/302
239	269	BC001401	gi|12655098|gb|BC001401.1|BC001401 Homo sapiens, Similar to sterile-alpha motif and leucine zipper containing kinase AZK, clone MGC:808, mRNA, complete cds	773	1571	0	396/398

Table 3
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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
240	270	S76617	gi|914203|gb|S76617.1|S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	38.2	2608	0.87	19/19
242	273	AK006144	gi|12839086|dbj|AK006144.1|AK006144 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700020B19, full insert sequence	323	1387	1E-86	233/255
243	276	X91656	gi|2125862|emb|X91656.1|MMSRP20 M.musculus Srp20 gene	494	13121	1E-138	262/265
247	236	BC002499	gi|12803360|gb|BC002499.1|BC002499 Homo sapiens, serine/threonine kinase 15, clone MGC:1605, mRNA, complete cds	640	2129	0	330/331
248	277	NM_003618	gi|4506376|ref|NM_003618.1| Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA	702	4380	0	361/362
249	278	NM_018492	gi|8923876|ref|NM_018492.1| Homo sapiens PDZ-binding kinase; T-cell originated protein kinase (TOPK), mRNA	779	1548	0	400/401
250	278	XM_005110	gi|12734111|ref|XM_005110.2| Homo sapiens PDZ-binding kinase; T-cell originated protein kinase (TOPK), mRNA	1003	1537	0	506/506
252	274	BC002466	gi|12803300|gb|BC002466.1|BC002466 Homo sapiens, v-raf murine sarcoma 3611 viral oncogene homolog 1, clone MGC:2356, mRNA, complete cds	1074	2451	0	575/581
253	280	XM_001729	gi|11423735|ref|XM_001729.1| Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) (AKT3), mRNA	751	1658	0	385/387
254	259	NM_002893	gi|13259504|ref|NM_002893.2| Homo sapiens retinoblastoma-binding protein 7 (RBBP7), mRNA	1164	1946	0	715/746
255	210	AB056798	gi|13365896|dbj|AB056798.1|AB056798 Macaca fascicularis brain cDNA clone:QflA-11110, full insert sequence	678	4521	0	435/461
256	213	AJ302649	gi|11140019|emb|AJ302649.1|DRE302649 Danio rerio mRNA for GABAA receptor betaZ2 subunit (gabaabeta2 gene)	42.1	2188	0.058	21/21

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
257	212	L27711	gi|808006|gb|L27711.1|HUMKAP1A Human protein phosphatase (KAP1) mRNA, complete cds	1057	844	0	550/553
258	214	NM_004336	gi|4757877|ref|NM_004336.1| Homo sapiens budding uninhibited by benzimidazoles 1 (yeast homolog) (BUB1), mRNA	1318	3446	0	694/701
260	216	NM_004300	gi|4757713|ref|NM_004300.1| Homo sapiens acid phosphatase 1, soluble (ACP1), transcript variant a, mRNA	985	2222	0	621/656
262	219	AK026166	gi|10438929|dbj|AK026166.1|AK026166 Homo sapiens cDNA: FLJ22513 fis, clone HRC12111, highly similar to HUMKUP Human Ku (p70/p80) subunit mRNA	1402	1813	0	838/871
263	252	BC004937	gi|13436283|gb|BC004937.1|BC004937 Homo sapiens, clone MGC:10779, mRNA, complete cds	898	1032	0	475/480
264	220	XM_006375	gi|12736706|ref|XM_006375.2| Homo sapiens glutathione S-transferase pi (GSTP1), mRNA	1316	737	0	693/703
265	218	BC001827	gi|12804774|gb|BC001827.1|BC001827 Homo sapiens, Similar to deoxythymidylate kinase (thymidylate kinase), clone MGC:3923, mRNA, complete cds	1259	1073	0	672/683
266	221	BC002900	gi|12804094|gb|BC002900.1|BC002900 Homo sapiens, Similar to proteasome (prosome, macropain) subunit, alpha type, 2, clone IMAGE:3942625, mRNA, partial cds	1217	867	0	699/728
267	226	AF064029	gi|4091894|gb|AF064029.1|AF064029 Helianthus tuberosus lectin 1 mRNA, complete cds	60	779	0.0000002	30/30
268	212	L27711	gi|808006|gb|L27711.1|HUMKAP1A Human protein phosphatase (KAP1) mRNA, complete cds	1257	844	0	694/705
269	223	XM_011470	gi|12732420|ref|XM_011470.1| Homo sapiens myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L) (MACS), mRNA	1029	2591	0	519/519
270	221	BC002900	gi|12804094|gb|BC002900.1|BC002900 Homo sapiens, Similar to proteasome (prosome, macropain) subunit, alpha type, 2, clone IMAGE:3942625, mRNA, partial cds	1330	867	0	724/739
271	206	BC002476	gi|12803316|gb|BC002476.1|BC002476 Homo sapiens, non-metastatic cells 2, protein (NM23B) expressed in, clone MGC:2212, mRNA, complete cds	1203	695	0	610/611

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SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
272	225	XM_007980	gi|12739602|ref|XM_007980.2| Homo sapiens membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase (PKMYT1), mRNA	904	1866	0	481/487
273	231	S50810	gi|262070|gb|S50810.1|S50810 {satellite DNA} [Drosophila melanogaster, Doc mobile element, Transposon, 1086 nt]	52	1086	0.00003	29/30
274	233	AF217396	gi|8132773|gb|AF217396.1|AF217396 Drosophila melanogaster clone 2G2 unknown mRNA	46.1	2007	0.004	23/23
275	232	L29057	gi|609636|gb|L29057.1|XELCADH Xenopus laevis (clone: XTCAD-1) cadherin gene, complete cds	40.1	4097	0.081	20/20
276	227	XM_008475	gi|11426657|ref|XM_008475.1| Homo sapiens KIAA0100 gene product (KIAA0100), mRNA	40.1	6962	0.32	20/20
277	229	M34230	gi|204651|gb|M34230.1|RATHPA1 Rat haptoglobin (Hp) gene, exons 1,2 and 3	56	3282	0.000002	28/28
278	230	AJ302649	gi|11140019|emb|AJ302649.1|DRE302649 Danio rerio mRNA for GABAA receptor betaZ2 subunit (gabaabeta2 gene)	50.1	2188	0.0002	25/25
279	239	NM_021158	gi|11056039|ref|NM_021158.1| Homo sapiens protein kinase domains containing protein similar to phosphoprotein C8FW (LOC57761), mRNA	710	2257	0	358/358
280	238	AX030958	gi|10278361|emb|AX030958.1|AX030958 Sequence 7 from Patent WO9800549	56	3828	0.000005	28/28
281	228	XM_010102	gi|11419709|ref|XM_010102.1| Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA	1469	1767	0	839/865
282	235	U00238	gi|404860|gb|U00238.1|U00238 Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds	1132	3600	0	653/677
283	237	NM_002753	gi|4506080|ref|NM_002753.1| Homo sapiens mitogen-activated protein kinase 10 (MAPK10), mRNA	733	2372	0	381/385
284	241	XM_006151	gi|12736568|ref|XM_006151.2| Homo sapiens similar to serine protease, umbilical endothelium (H. sapiens) (LOC63320), mRNA	979	1640	0	494/494
285	242	BC004215	gi|13278917|gb|BC004215.1|BC004215 Homo sapiens, eukaryotic translation elongation factor 1 gamma, clone MGC:4501, mRNA, complete cds	1106	3373	0	578/585

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
286	243	NM_000455	gi|4507270|ref|NM_000455.1| Homo sapiens serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11), mRNA	1243	2158	0	651/660
287	258	XM_004842	gi|12733228|ref|XM_004842.2| Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA	682	3715	0	381/387
288	261	NM_020197	gi|9910273|ref|NM_020197.1| Homo sapiens HSKM-B protein (HSKM-B), mRNA	561	1694	1E-158	346/355
289	260	XM_001416	gi|12719345|ref|XM_001416.2| Homo sapiens similar to ribosomal protein S6 kinase, 90kD, polypeptide 1 (H. sapiens) (LOC65290), mRNA	517	2966	1E-145	277/284
290	236	BC002499	gi|12803360|gb|BC002499.1|BC002499 Homo sapiens, serine/threonine kinase 15, clone MGC:1605, mRNA, complete cds	618	2129	1E-175	358/366
293	246	XM_004679	gi|11419466|ref|XM_004679.1| Homo sapiens cyclin-dependent kinase 5 (CDK5), mRNA	383	987	1E-104	214/224
294	245	XM_005258	gi|11426310|ref|XM_005258.1| Homo sapiens serum/glucocorticoid regulated kinase-like (SGKL), mRNA	902	2391	0	463/466
295	248	XM_008654	gi|12740227|ref|XM_008654.2| Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4), mRNA	662	3576	0	369/374
296	129	BC002364	gi|12803120|gb|BC002364.1|BC002364 Homo sapiens, non-POU-domain-containing, octamer-binding, clone MGC:8677, mRNA, complete cds	688	2645	0	347/347
298	2	NM_004443	gi|4758287|ref|NM_004443.1| Homo sapiens EphB3 (EPHB3) mRNA	533	3805	1E-150	297/301
299	254	XM_002383	gi|11429253|ref|XM_002383.1| Homo sapiens activin A receptor, type I (ACVR1), mRNA	571	2832	1E-161	333/340
300	249	BC000633	gi|12653696|gb|BC000633.1|BC000633 Homo sapiens, TTK protein kinase, clone MGC:865, mRNA, complete cds	537	2993	1E-151	396/419
301	2	NM_004443	gi|4758287|ref|NM_004443.1| Homo sapiens EphB3 (EPHB3) mRNA	795	3805	0	453/467
302	224	XM_005116	gi|12734122|ref|XM_005116.2| Homo sapiens protein tyrosine kinase 2 beta (PTK2B), mRNA	470	3396	1E-131	252/259

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
303	222	AB056389	gi|13358639|dbj|AB056389.1|AB056389 Macaca fascicularis brain cDNA, clone:QflA-12365	196	2038	9E-49	129/141

Table 3
Blast Search Results

SEQ ID NO	CID	GenBank Accession No.	HitDesc	Score	Length	Expect	Identities
304	208	BC002921	gi|12804134|gb|BC002921.1|BC002921 Homo sapiens, Similar to protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs, clone MGC:10333, mRNA, complete cds	446	2349	1E-123	260/274
305	250	XM_004079	gi|11417431|ref|XM_004079.1| Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA	525	1719	1E-147	275/280
306	251	XM_004306	gi|11418576|ref|XM_004306.1| Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA	317	7375	4E-85	160/160
307	252	BC004937	gi|13436283|gb|BC004937.1|BC004937 Homo sapiens, clone MGC:10779, mRNA, complete cds	975	1032	0	567/582
308	253	NM_006293	gi|5454141|ref|NM_006293.1| Homo sapiens TYRO3 protein tyrosine kinase (TYRO3), mRNA	823	4364	0	457/466
309	257	X71765	gi|402221|emb|X71765.1|PFCAATPAS P. falciparum gene for Ca2+ - ATPase	38.2	5477	1.4	19/19

Table 4
Patient Data

Patient ID	Path Report ID	Group	Anatom Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion
15	21	III	Ascending colon	4.0	T3	G2	extending into subserosal adipose tissue
52	71	II	Ascending colon	9.0	T3	G3	Invasion through muscularis propria, subserosal involvement; ileocec. valve involvement
121	140	II	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving submucosa of urinary bladder
125	144	II	Cecum	6	T3	G2	Invasion through the muscularis propria into suserosal adipose tissue. Ileocecal junction.
128	147	III	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into percolonic fat
130	149		Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue
133	152	II	Rectum	5.0	T3	G2	Invasion through muscularis propria into non-peritonealized pericolic tissue; gross configuration is annular.
141	160	IV	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolonic adipose tissue, but not through serosa. Arising from tubular adenoma.

Table 4
Patient Data

Patient ID	Path Report ID	Group	Anatom Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion
156	175	III	Hepatic flexure	3.8	T3	G2	Invasion through mucsularis propria into subserosa/pericolic adipose, no serosal involvement. Gross configuration annular.
228	247	III	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectoal adipose, and serosa
264	283	II	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.
266	285	III	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolonic adipose, extends to serosa.
268	287	I	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy
278	297	III	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.
295	314	II	Ascending colon	5.0	T3	G2	Invasion through muscularis propria into percolic adipose tissue.
339	358	II	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa

Table 4
Patient Data

Patient ID	Path Report ID	Group	Anatom Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion
341	360	II	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.
356	375	II	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.
360	412	III	Ascending colon	4.3	T3	G2	Invasion thru muscularis propria to pericolonic fat
392	444	IV	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.
393	445	II	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.
413	465	IV	Ascending colon	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.
505	383	IV		7.5 cm max dim	T3	G2	Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved
517	395	IV	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolonic fat.
534	553	II	Ascending colon	12	T3	G3	Invasion through the muscularis propria involving pericolic fat. Serosa free of tumor.

Table 4
Patient Data

Patient ID	Path Report ID	Group	Anatom Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion
546	565	IV	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending
577	596	II	Cecum	11.5	T3	G2	Invasion through the bowel wall, into suberosal adipose. Serosal surface free of tumor.

Table 4
Patient Data

Patient ID	Path Report ID	Group	Anatom Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion
695	714	II	Cecum	14	T3	G2	extending through bowel wall into serosal fat
784	803	IV	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues
786	805	IV	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface
791	810	IV	Ascending colon	5.8	T3	G3	through the muscularis propria into pericolic fat
888	908	IV	Ascending colon	2.0	T2	G1	into muscularis propria
889	909	IV	Cecum	4.8	T3	G2	through muscularis propria int subserosal tissue

Table 4
Patient Data

Patient ID	Lymphnode Met	Incidence Lymphnode Met	Regional Lympnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
15	positive	3/8	N1	negative		MX	invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen
52	negative	0/12	N0	negative		M0	Hyperplastic polyp in appendix.
121	negative	0/34	N0	negative		M0	Perineural invasion; donut anastomosis negative. One tubulovillous and one tubular adenoma with no high grade dysplasia.
125	negative	0/19	N0	negative		M0	patient history of metastatic melanoma
128	positive	1/5	N1	negative		M0	
130	positive	10/24	N2	negative		M1	
133	negative	0/9	N0	negative		M0	Small separate tubular adenoma (0.4 cm)
141	positive	7/21	N2	positive (Liver)	adenocarcinoma consistant with primary	M1	Perineural invasion identified adjacent to metastatic adenocarcinoma.

Table 4
Patient Data

Patient ID	Lymphnode Met	Incidence Lymphnode Met	Regional Lympnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
156	positive	2/13	N1	negative		M0	Separate tubolovillous and tubular adenomas
228	positive	1/8	N1	negative		MX	Hyperplastic polyps
264	negative	0/10	N0	negative		M0	Tubulovillous adenoma with high grade dysplasia
266	negative	0/15	N1	positive (Mesenteric deposit)	0.4 cm, may represent lymph node completely replaced by tumor	MX	
268	negative	0/12	N0	negative		M0	
278	positive	7/10	N2	negative		M0	Descending colon polyps, no HGD or carcinoma identified.
295	negative	0/12	N0	negative		M0	Melanosis coli and diverticular disease.
339	negative	0/6	N0	negative		M0	1 hyperplastic polyp identified

Table 4
Patient Data

Patient ID	Lymphnode Met	Incidence Lymphnode Met	Regional Lympnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
341	negative	0/4	N0	negative		MX	
356	negative	0/4	N0	negative		M0	
360	positive	1/5	N1	negative		M0	Two mucosal polyps
392	positive	1/6	N1	positive (Liver)	Macrovesicular and microvesicular steatosis	M1	Tumor arising at prior ileocolic surgical anastomosis.
393	negative	0/21	N0	negative		M0	
413	negative	0/7	N0	positive (Liver)	adenocarcinoma in multiple slides	M1	rediagnosis of oophorectomy path to metastatic colon cancer.
505	positive	2/17	N1	positive (Liver)	moderately differentiated adenocarcinoma, consistant with primary	M1	Anatomical location of primary not notated in report. Evidence of chronic colitis.
517	positive	6/6	N2	negative		M0	No mention of distant met in report
534	negative	0/8	N0	negative		M0	Omentum with fibrosis and fat necrosis. Small bowel with acute and chronic serositis, focal abscess and adhesions.

Table 4
Patient Data

Patient ID	Lymphnode Met	Incidence Lymphnode Met	Regional Lympnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
546	positive	6/12	N2	positive (Liver)	metastatic adenocarcinoma	M1	
577	negative	0/58	N0	negative		M0	Appendix dilated and fibrotic, but not involved by tumor

Table 4
Patient Data

Patient ID	Lymphnode Met	Incidence Lymphnode Met	Regional Lympnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
695	negative	0/22	N0	negative		MX	tubular adenoma and hyperplstic polyps present, moderately differentiated adenoma with mucinous diferentiation (% not stated)
784	positive	5/17	N2	positive (Liver)		M1	invasive poorly differentiated adenosquamous carcinoma
786	negative	0/12	N0	positive (Liver)		M1	moderately differentiated invasive adenocarcinoma
791	positive	13/25	N2	positive (Liver)		M1	poorly differentiated invasive colonic adenocarcinoma
888	positive	3/21	N0	positive (Liver)		M1	well- to moderately-differentiated adenocarcinoma; this patient has tumors of the ascending colon and the sigmoid colon
889	positive	1/4	N1	positive (Liver)		M1	moderately differentiated adenocarcinoma

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
27	1	M00023371A:G03	1:85
195	1	M00001489B:G04	1:227
212	1	M00026888A:A03	1:244
335	1	M00001558C:B06	1:367
511	1	M00003852B:C01	2:191
538	1	M00022009A:A12	2:218
599	1	M00001374A:A06	2:279
943	1	M00001341B:A11	3:271
1048	1	M00007965C:G08	3:376
1160	1	M00022140A:E11	4:136
1176	1	M00022180D:E11	4:152
1195	1	M00001675B:G05	4:171
1203	1	M00003853B:G11	4:179
1252	1	M00022742A:F08	4:228
1266	1	M00026900D:F02	4:242
1605	1	M00001496A:G03	5:229
1648	1	M00001393D:F01	5:272
1793	1	M00023283C:C06	6:65
1927	1	M00007985A:B08	6:199
1933	1	M00007985B:A03	6:205
2332	1	M00026903D:D11	7:252
2404	1	M00006883D:H12	7:324
2633	1	M00007987D:D04	8:201
2659	1	M00023431B:A01	8:227
2662	1	M00023363C:A04	8:230
2799	1	M00004031B:D12	8:367
2889	1	M00003814C:C11	9:105
2917	1	M00007935D:A05	9:133
3005	1	M00021956B:A09	9:221
3204	1	M00027066B:E09	10:68
3296	1	M00022215C:A10	10:160
3313	1	M00003961B:H05	10:177
3519	1	M00005360A:A07	10:383
3665	1	M00001600C:B11	11:177
3748	1	M00001402B:C12	11:260
3974	1	M00022168B:F02	12:134
4040	1	M00008049B:A12	12:200
8594	2	RG:742775:10011:A07	1:178
8630	2	I:2458926:03B01:C07	1:214
8788	2	I:3229778:02B01:B07	1:372
8840	2	I:1857563:05B02:D01	2:72
9042	2	I:4072558:12B01:A07	2:274
9191	2	I:1421929:05A01:D02	3:71
9349	2	I:1723834:01A01:C02	3:229
9478	2	I:1817434:02B01:C02	3:358
9489	2	I:1750782:02A01:A08	3:369
9547	2	I:1297179:05A02:F02	4:75

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
9684	2	I:1443877:03B02:B08	4:212
9724	2	I:1384823:01B02:F08	4:252
9739	2	I:2902903:12A02:F02	4:267
9809	2	I:2152363:04A02:A08	4:337
10000	2	RG:813679:10011:H03	5:176
10006	2	RG:759927:10011:C09	5:182
10153	2	I:1712592:04A01:E03	5:329
10168	2	I:2615513:04B01:D09	5:344
10200	2	I:1702266:02B01:D09	5:376
10299	2	I:2825369:07A02:F09	6:123
10394	2	I:1450639:03B02:E09	6:218
10426	2	I:2499976:01B02:E09	6:250
10600	2	I:1749883:05B01:D04	7:72
10614	2	I:1516301:05B01:C10	7:86
10621	2	I:1298021:05A01:G10	7:93
10744	2	I:1613615:03B01:D10	7:216
10877	2	I:1395918:04A01:G10	7:349
10956	2	I:1600586:05B02:F04	8:76
10984	2	I:1666080:07B02:D04	8:104
11017	2	I:1633286:06A02:E04	8:137
11019	2	I:1609538:06A02:F04	8:139
11035	2	I:1630804:06A02:F10	8:155
11223	2	I:1749417:04A02:D10	8:343
11245	2	I:1809385:02A02:G04	8:365
11258	2	I:1854245:02B02:E10	8:378
11445	2	I:1854558:03A01:C11	9:213
11569	2	I:1509602:04A01:A11	9:337
11739	2	I:1699587:06A02:F11	10:155
11838	2	I:2840195:01B02:G11	10:254
11908	2	I:2914719:04B02:B05	10:324
11923	2	I:2239819:04A02:B11	10:339
12001	2	I:2483109:05A01:A06	11:65
12007	2	I:2499479:05A01:D06	11:71
12013	2	I:2675481:05A01:G06	11:77
12104	2	RG:773612:10011:D06	11:168
12270	2	I:2914605:04B01:G06	11:334
12513	2	I:2079906:01A02:A06	12:225
12519	2	I:1810640:01A02:D06	12:231
16933	3	I:1963753:18B01:E07	1:122
17035	3	RG:166410:10006:F01	1:171
17059	3	I:1920650:16A01:B01	1:195
17068	3	I:1923769:16B01:F01	1:204
17069	3	I:901317:16A01:G01	1:205
17075	3	I:3518380:16A01:B07	1:211
17171	3	RG:666323:10010:B07	1:307
17385	3	RG:244132:10007:E01	2:169
17386	3	RG:2117694:10016:E01	2:170

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
17399	3	RG:241029:10007:D07	2:183
17459	3	I:2056395:13A02:B07	2:243
17533	3	RG:1555877:10013:G07	2:317
17696	3	I:1923490:18B01:H08	3:128
17730	3	RG:526536:10002:A02	3:162
17742	3	RG:612874:10002:G02	3:174
17746	3	RG:530002:10002:A08	3:178
17836	3	RG:29739:10004:F02	3:268
17964	3	I:1920522:15B02:F02	4:44
18089	3	RG:244601:10007:E02	4:169
18100	3	RG:2048081:10016:B08	4:180
18102	3	RG:2097294:10016:C08	4:182
18240	3	RG:1927470:10015:H08	4:320
18331	3	I:1926006:15A01:F09	5:59
18379	3	I:2359588:18A01:F03	5:107
18389	3	I:986558:18A01:C09	5:117
18408	3	I:970933:14B01:D03	5:136
18445	3	RG:180296:10006:G03	5:173
18488	3	I:1743234:16B01:D09	5:216
18552	3	RG:25258:10004:D09	5:280
18580	3	RG:985973:10012:B09	5:308
18801	3	RG:203031:10007:A09	6:177
18804	3	RG:2055807:10016:B09	6:180
18856	3	I:605019:13B02:D03	6:232
18886	3	RG:43296:10005:C03	6:262
18903	3	RG:301608:10008:D09	6:279
18904	3	RG:45623:10005:D09	6:280
18921	3	RG:1461567:10013:E03	6:297
18942	3	RG:1895716:10015:G09	6:318
18985	3	I:1402615:09A02:E03	6:361
19067	3	I:2054678:19A01:F10	7:91
19120	3	I:956077:14B01:H04	7:144
19175	3	I:750899:16A01:D04	7:199
19189	3	I:620494:16A01:C10	7:213
19229	3	I:2060725:13A01:G10	7:253
19264	3	RG:35892:10004:H10	7:288
19374	3	I:1758241:15B02:G04	8:46
19428	3	I:1965257:18B02:B04	8:100
19590	3	RG:43534:10005:C04	8:262
19600	3	RG:110764:10005:H04	8:272
19603	3	RG:278409:10008:B10	8:275
19604	3	RG:41097:10005:B10	8:276
19629	3	RG:1552386:10013:G04	8:301
19642	3	RG:1838677:10015:E10	8:314
19766	3	I:1996180:19B01:C11	9:86
19816	3	I:1431819:14B01:D05	9:136
19821	3	I:1833191:14A01:G05	9:141

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
19822	3	I:1227385:14B01:G05	9:142
19835	3	I:2055926:14A01:F11	9:155
19950	3	RG:32281:10004:G05	9:270
19962	3	RG:27403:10004:E11	9:282
19971	3	RG:665682:10010:B05	9:291
20102	3	I:2759046:19B02:C05	10:70
20196	3	RG:2012168:10016:B05	10:164
20280	3	I:1960722:13B02:D11	10:248
20303	3	RG:343821:10008:H05	10:271
20315	3	RG:323425:10008:F11	10:283
20506	3	I:1969044:18B01:E12	11:122
20586	3	I:659143:16B01:E06	11:202
20691	3	RG:669110:10010:B12	11:307
20703	3	RG:740831:10010:H12	11:319
20775	3	I:1968921:15A02:D06	12:39
20878	3	I:998612:14B02:G06	12:142
20915	3	RG:208954:10007:B12	12:179
20940	3	I:1967543:16B02:F06	12:204
21017	3	RG:306813:10008:E12	12:281
21025	3	RG:1353123:10013:A06	12:289
21068	3	I:549299:17B02:F06	12:332
21160	4	RG:1996901:20003:D01	1:104
21207	4	M00056483D:G07	1:151
21294	4	M00042439D:C11	1:238
21354	4	RG:781507:10011:E01	1:298
21518	4	RG:1374447:20004:G01	2:110
21544	4	M00056908A:H05	2:136
21589	4	M00054777D:E09	2:181
21674	4	RG:2002384:20003:E01	2:266
21705	4	RG:1651303:10014:E01	2:297
21732	4	M00054538C:C01	2:324
21763	4	M00056622B:F12	2:355
21769	4	M00056632B:H10	2:361
21784	4	M00055423A:C07	2:376
21812	4	M00056308A:F02	3:52
21884	4	RG:2006302:20003:F08	3:124
21921	4	M00054639D:F05	3:161
21983	4	M00057081B:H03	3:223
22023	4	M00056533D:G07	3:263
22027	4	M00056534C:E08	3:267
22043	4	M00056585B:F04	3:283
22060	4	RG:785846:10011:F02	3:300
22072	4	RG:781028:10011:D08	3:312
22254	4	M00056918C:F09	4:142
22285	4	M00054742C:B12	4:173
22299	4	M00054806B:G03	4:187
22366	4	M00056350B:B03	4:254

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
22375	4	M00056728C:G02	4:263
22405	4	RG:1637619:10014:C02	4:293
22415	4	RG:1674393:10014:H02	4:303
22419	4	RG:1635546:10014:B08	4:307
22498	4	M00056250C:B02	5:34
22619	4	M00056500C:A07	5:155
22633	4	M00054647A:A09	5:169
22678	4	M00057231A:G04	5:214
22724	4	RG:1861510:20001:B03	5:260
22775	4	RG:417109:10009:D09	5:311
22783	4	RG:487171:10009:H09	5:319
23103	4	M00056810A:A02	6:287
23179	4	M00056645C:D11	6:363
23183	4	M00056646B:F07	6:367
23189	4	M00056679B:H03	6:373
23286	4	RG:1996788:20003:C10	7:118
23337	4	M00054650D:E04	7:169
23371	4	M00057044D:G03	7:203
23373	4	M00057046A:G09	7:205
23380	4	M00057241C:F03	7:212
23394	4	M00042756A:H02	7:226
23471	4	RG:471154:10009:H04	7:303
23514	4	M00054520A:D04	7:346
23803	4	M00056812D:A08	8:283
23813	4	RG:1638979:10014:C04	8:293
23984	4	RG:2051667:20003:H05	9:112
24185	4	RG:432960:10009:E11	9:313
24186	4	RG:785368:10011:E11	9:314
24297	4	M00055209C:B07	10:73
24358	4	M00056937C:C10	10:134
24394	4	M00056992C:F12	10:170
24423	4	M00057126C:B03	10:199
24429	4	M00057127B:B09	10:205
24515	4	RG:1630930:10014:B05	10:291
24519	4	RG:1645945:10014:D05	10:295
24700	4	RG:2006592:20003:F12	11:124
24713	4	M00056478D:B07	11:137
24728	4	M00056227B:G06	11:152
24806	4	M00042770D:G04	11:230
24855	4	M00056619A:H02	11:279
24866	4	RG:742764:10011:A06	11:290
24867	4	RG:364972:10009:B06	11:291
24883	4	RG:376554:10009:B12	11:307
24900	4	M00054500D:C08	11:324
24944	4	M00054971D:D07	11:368
25021	4	M00055258B:D12	12:93
25095	4	M00054769A:E05	12:167

Table 5
Array Coordinates

SpotID	Chip Num	Sample Name or Clone Name	Coords
25161	4	M00055435B:A12	12:233
25203	4	M00056822A:E08	12:275
25212	4	RG:2006592:20003:F12	12:284
25219	4	RG:1631867:10014:B06	12:291
25305	4	M00056707D:D05	12:377
25309	4	M00056709B:D03	12:381
25332	4	M00055583C:B07	1:55
25337	4	M00056301D:A04	1:60
25393	2	I:2606813:04A02:B12	12:339
25430	2	I:1931371:02B02:D12	12:376

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
1	114	2889	51.5	45.5	12.1	0.0	33
2	123	1833	51.5	45.5	24.2	0.0	33
2	123	2404	60.6	48.5	9.1	0.0	33
3	114	2889	51.5	45.5	12.1	0.0	33
4	1	17957	24.2	24.2	18.2	3.0	33
5	2	19822	54.5	39.4	18.2	3.0	33
6	3	9547	54.5	33.3	6.1	0.0	33
7	4	10621	72.7	54.5	9.1	0.0	33
9	6	9724	54.5	48.5	33.3	0.0	33
10	7	10877	78.8	69.7	21.2	0.0	33
11	8	18985	60.6	60.6	24.2	0.0	33
12	9	9191	75.8	69.7	42.4	0.0	33
13	10	19816	39.4	33.3	21.2	0.0	33
14	11	9684	42.4	24.2	9.1	0.0	33
15	12	10394	63.6	51.5	30.3	0.0	33
16	13	10314	33.3	27.3	12.1	0.0	33
17	14	11569	84.8	78.8	66.7	0.0	33
18	15	10614	66.7	54.5	33.3	3.0	33
19	167	25332	54.5	42.4	12.1	0.0	33
20	16	10956	51.5	39.4	12.1	0.0	33
21	17	11019	42.4	33.3	6.1	0.0	33
22	18	10744	66.7	66.7	51.5	6.1	33
23	19	11035	48.5	39.4	39.4	0.0	33
24	20	11017	33.3	24.2	15.2	0.0	33
25	21	10984	54.5	45.5	30.3	3.0	33
26	22	11739	48.5	36.4	18.2	0.0	33
27	23	10200	24.2	9.1	0.0	0.0	33
28	24	10153	36.4	30.3	21.2	0.0	33
29	25	9349	54.5	42.4	30.3	0.0	33
30	26	18488	21.2	21.2	21.2	9.1	33
31	170	22498	51.5	33.3	15.2	0.0	33
32	27	11223	78.8	63.6	24.2	0.0	33
33	28	10600	33.3	24.2	3.0	3.0	33
34	29	9489	27.3	21.2	18.2	0.0	33
35	30	19374	33.3	24.2	15.2	6.1	33
36	31	11245	27.3	18.2	12.1	0.0	33
37	32	12519	39.4	36.4	12.1	0.0	33
38	33	9478	57.6	33.3	9.1	0.0	33
39	34	19821	36.4	21.2	12.1	3.0	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
40	35	11258	27.3	18.2	12.1	0.0	33
41	36	11445	54.5	51.5	42.4	0.0	33
42	37	8840	57.6	36.4	9.1	0.0	33
43	38	17964	45.5	33.3	6.1	0.0	33
44	39	17059	48.5	30.3	9.1	0.0	33
45	41	17696	81.8	72.7	24.2	0.0	33
46	42	17068	39.4	30.3	3.0	0.0	33
47	43	18331	48.5	36.4	9.1	0.0	33
48	44	25430	45.5	18.2	6.1	0.0	33
49	45	20280	42.4	30.3	3.0	0.0	33
50	46	16933	27.3	21.2	18.2	6.1	33
51	47	19428	39.4	36.4	27.3	0.0	33
52	48	20940	27.3	21.2	12.1	3.0	33
53	49	20775	36.4	33.3	12.1	9.1	33
54	50	20506	24.2	15.2	3.0	3.0	33
56	53	19766	57.6	51.5	30.3	3.0	33
57	54	19067	45.5	42.4	36.4	6.1	33
58	55	19835	45.5	39.4	12.1	3.0	33
59	56	17459	81.8	72.7	51.5	0.0	33
60	58	19229	33.3	12.1	0.0	0.0	33
61	59	12513	57.6	33.3	15.2	3.0	33
62	60	9809	78.8	66.7	42.4	0.0	33
63	63	11923	72.7	69.7	60.6	3.0	33
64	64	18379	36.4	36.4	27.3	3.0	33
65	65	8630	48.5	42.4	24.2	6.1	33
66	66	12001	66.7	51.5	24.2	0.0	33
67	67	12007	54.5	42.4	24.2	0.0	33
68	68	10426	51.5	39.4	18.2	0.0	33
70	71	10168	36.4	24.2	12.1	0.0	33
71	74	12013	39.4	24.2	9.1	0.0	33
73	100	943	54.5	27.3	6.1	3.0	33
74	105	3748	100.0	84.8	36.4	0.0	33
75	106	3750	39.4	36.4	27.3	3.0	33
76	104	1648	57.6	48.5	27.3	9.1	33
77	75	20102	69.7	51.5	30.3	0.0	33
78	76	10299	57.6	42.4	12.1	0.0	33
79	77	11838	54.5	48.5	39.4	0.0	33
80	78	9739	81.8	78.8	63.6	0.0	33
81	79	12270	48.5	39.4	27.3	0.0	33
82	80	11908	48.5	24.2	0.0	0.0	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
83	81	8788	33.3	12.1	9.1	0.0	33
84	109	195	57.6	21.2	3.0	0.0	33
85	110	1605	81.8	66.7	9.1	0.0	33
86	111	335	75.8	54.5	12.1	0.0	33
87	121	3519	39.4	21.2	6.1	0.0	33
88	118	2799	54.5	36.4	15.2	0.0	33
89	41	1252	81.8	66.7	21.2	0.0	33
90	139	2662	69.7	54.5	12.1	0.0	33
91	83	17075	48.5	18.2	0.0	0.0	33
92	85	9042	72.7	57.6	12.1	0.0	33
93	117	3313	48.5	24.2	3.0	0.0	33
94	113	1195	60.6	42.4	0.0	0.0	33
95	87	21068	39.4	33.3	21.2	6.1	33
96	88	18856	63.6	42.4	3.0	0.0	33
97	89	19189	54.5	36.4	0.0	0.0	33
98	125	1048	66.7	66.7	42.4	3.0	33
99	128	2633	48.5	27.3	9.1	0.0	33
100	127	1933	66.7	48.5	6.1	0.0	33
101	129	4040	54.5	42.4	9.1	0.0	33
102	130	2224	21.2	15.2	9.1	0.0	33
104	136	3974	57.6	51.5	27.3	0.0	33
106	5	1176	75.8	57.6	12.1	0.0	33
107	137	3296	51.5	36.4	9.1	0.0	33
108	138	1793	57.6	30.3	6.1	0.0	33
109	141	2659	72.7	57.6	15.2	0.0	33
110	90	20586	24.2	18.2	12.1	3.0	33
111	145	3204	48.5	48.5	48.5	9.1	33
112	91	19175	63.6	33.3	3.0	0.0	33
113	92	18489	66.7	60.6	18.2	3.0	33
114	93	17069	60.6	18.2	3.0	0.0	33
116	100	943	54.5	27.3	6.1	3.0	33
118	123	1833	51.5	45.5	24.2	0.0	33
118	123	2404	60.6	48.5	9.1	0.0	33
119	94	19120	45.5	30.3	21.2	3.0	33
120	95	18408	84.8	54.5	21.2	0.0	33
121	96	18389	24.2	24.2	21.2	3.0	33
122	98	20878	42.4	42.4	36.4	3.0	33
123	103	599	84.8	84.8	63.6	0.0	33
124	103	599	84.8	84.8	63.6	0.0	33
125	133	538	69.7	66.7	42.4	0.0	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
126	133	538	69.7	66.7	42.4	0.0	33
130	115	511	66.7	60.6	42.4	3.0	33
131	106	3750	39.4	36.4	27.3	3.0	33
132	113	1195	60.6	42.4	0.0	0.0	33
133	113	1195	60.6	42.4	0.0	0.0	33
134	106	3750	39.4	36.4	27.3	3.0	33
135	116	1203	51.5	48.5	39.4	6.1	33
136	117	3313	48.5	24.2	3.0	0.0	33
138	123	1833	51.5	45.5	24.2	0.0	33
138	123	2404	60.6	48.5	9.1	0.0	33
140	140	27	42.4	24.2	12.1	0.0	33
141	143	1266	60.6	54.5	48.5	3.0	33
142	121	3519	39.4	21.2	6.1	0.0	33
143	121	3519	39.4	21.2	6.1	0.0	33
144	139	2662	69.7	54.5	12.1	0.0	33
145	112	3665	78.8	69.7	18.2	0.0	33
147	166	25161	60.6	36.4	6.1	0.0	33
148	167	25332	54.5	42.4	12.1	0.0	33
149	169	24233	21.2	15.2	3.0	3.0	33
150	30	24728	39.4	21.2	0.0	0.0	33
151	170	22498	51.5	33.3	15.2	0.0	33
152	171	25337	78.8	72.7	24.2	0.0	33
152	171	25339	27.3	27.3	27.3	0.0	33
153	171	25337	78.8	72.7	24.2	0.0	33
153	171	25339	27.3	27.3	27.3	0.0	33
154	172	21812	60.6	39.4	0.0	0.0	33
155	147	21294	54.5	33.3	3.0	0.0	33
156	149	23394	42.4	9.1	3.0	0.0	33
157	150	24806	30.3	9.1	0.0	3.0	33
159	173	22366	81.8	60.6	18.2	0.0	33
161	175	24713	21.2	18.2	0.0	0.0	33
162	176	21207	42.4	39.4	30.3	0.0	33
163	177	22619	69.7	45.5	3.0	0.0	33
164	178	22023	39.4	27.3	3.0	0.0	33
165	179	22027	42.4	36.4	21.2	9.1	33
166	180	22043	42.4	30.3	9.1	0.0	33
168	182	24855	33.3	21.2	6.1	0.0	33
169	183	21763	75.8	57.6	3.0	0.0	33
170	184	21769	27.3	15.2	0.0	0.0	33
171	185	23179	36.4	27.3	3.0	0.0	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
171	185	23181	33.3	15.2	3.0	0.0	33
172	185	23179	36.4	27.3	3.0	0.0	33
172	185	23181	33.3	15.2	3.0	0.0	33
173	186	23183	39.4	33.3	18.2	3.0	33
174	187	23189	63.6	51.5	9.1	0.0	33
176	189	25309	30.3	18.2	3.0	0.0	33
177	190	22375	42.4	24.2	15.2	3.0	33
179	192	23103	27.3	15.2	3.0	0.0	33
180	193	23803	57.6	45.5	15.2	0.0	33
181	194	25203	72.7	54.5	15.2	0.0	33
182	195	21544	33.3	27.3	9.1	0.0	33
183	196	22254	39.4	12.1	0.0	0.0	33
184	197	24358	42.4	30.3	18.2	0.0	33
185	197	24358	42.4	30.3	18.2	0.0	33
190	199	24394	42.4	30.3	3.0	0.0	33
191	199	24394	42.4	30.3	3.0	0.0	33
192	200	23371	81.8	66.7	12.1	0.0	33
193	176	23373	84.8	66.7	15.2	0.0	33
194	201	21983	75.8	75.8	57.6	0.0	33
198	204	24429	39.4	27.3	3.0	0.0	33
200	206	22678	57.6	36.4	3.0	0.0	33
201	207	23380	63.6	36.4	3.0	0.0	33
202	152	24900	84.8	72.7	6.1	3.0	33
204	151	23514	57.6	45.5	3.0	0.0	33
205	151	23514	57.6	45.5	3.0	0.0	33
206	153	21732	54.5	30.3	0.0	0.0	33
207	154	21921	57.6	36.4	0.0	0.0	33
208	155	22633	60.6	36.4	6.1	0.0	33
209	156	23337	54.5	30.3	0.0	0.0	33
209	156	23339	24.2	21.2	21.2	0.0	33
210	157	22285	69.7	60.6	15.2	0.0	33
211	158	25095	54.5	39.4	6.1	0.0	33
212	159	21589	63.6	57.6	18.2	15.2	33
213	160	22299	66.7	45.5	15.2	0.0	33
214	161	21952	27.3	27.3	27.3	6.1	33
215	162	24944	48.5	30.3	9.1	0.0	33
217	195	24297	24.2	24.2	15.2	0.0	33
218	164	25021	66.7	48.5	9.1	0.0	33
220	65	21784	27.3	15.2	12.1	0.0	33
222	124	2917	51.5	30.3	12.1	0.0	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
223	126	1927	69.7	45.5	15.2	0.0	33
224	132	3005	93.9	60.6	12.1	0.0	33
225	291	1160	75.8	63.6	9.1	0.0	33
226	142	212	42.4	30.3	15.2	0.0	33
227	144	2332	48.5	18.2	6.1	0.0	33
228	115	511	66.7	60.6	42.4	3.0	33
230	255	24867	54.5	48.5	33.3	0.0	33
231	262	23471	66.7	42.4	15.2	0.0	33
232	256	24883	54.5	30.3	6.1	0.0	33
233	263	22783	24.2	15.2	9.1	3.0	33
234	265	17746	51.5	27.3	3.0	0.0	33
235	264	17730	63.6	48.5	18.2	3.0	33
236	266	17742	51.5	33.3	3.0	0.0	33
239	269	17171	30.3	24.2	15.2	0.0	33
240	270	20691	21.2	18.2	15.2	3.0	33
242	273	19997	21.2	21.2	21.2	9.1	33
243	276	24866	45.5	36.4	12.1	0.0	33
247	236	21354	24.2	6.1	0.0	3.0	33
248	277	22072	45.5	45.5	39.4	6.1	33
249	278	24186	39.4	33.3	18.2	0.0	33
250	278	22060	42.4	33.3	24.2	3.0	33
252	274	20703	69.7	54.5	12.1	0.0	33
253	280	18580	24.2	21.2	21.2	6.1	33
254	259	24185	48.5	30.3	3.0	0.0	33
255	210	17184	27.3	24.2	24.2	0.0	33
256	213	21518	36.4	30.3	24.2	3.0	33
257	212	21025	51.5	45.5	24.2	0.0	33
258	214	18921	30.3	18.2	9.1	0.0	33
260	216	19629	63.6	45.5	9.1	0.0	33
262	219	25219	51.5	33.3	6.1	0.0	33
263	252	22419	63.6	60.6	18.2	0.0	33
264	220	23813	63.6	45.5	3.0	0.0	33
265	218	24515	81.8	66.7	15.2	0.0	33
266	221	24519	57.6	39.4	3.0	3.0	33
267	226	22724	63.6	39.4	6.1	0.0	33
268	212	22405	48.5	45.5	30.3	3.0	33
269	223	21711	24.2	24.2	24.2	3.0	33
270	221	22415	48.5	24.2	6.1	0.0	33
271	206	21705	66.7	54.5	6.1	0.0	33
272	225	19642	33.3	27.3	18.2	12.1	33

Table6
Microarray Data

SEQ ID NO	CID	SpotID	>=2x	>=2.5x	>=5x	<=halfx	Num ratio
273	231	21162	54.5	39.4	24.2	6.1	33
273	231	21674	60.6	48.5	30.3	6.1	33
273	231	29993	50.0	17.9	10.7	0.0	28.0
274	233	24700	60.6	39.4	12.1	0.0	33
274	233	25212	66.7	45.5	12.1	0.0	33
274	233	33531	57.1	42.9	0.0	0.0	28
275	232	21884	54.5	36.4	21.2	3.0	33
275	232	22396	48.5	36.4	15.2	3.0	33
275	232	30715	39.3	17.9	3.6	0.0	28
276	227	18942	81.8	78.8	57.6	0.0	33
277	229	23286	69.7	45.5	15.2	0.0	33
277	229	23798	66.7	45.5	12.1	0.0	33
277	229	32117	50.0	32.1	14.3	0.0	28
278	230	21160	24.2	18.2	18.2	6.1	33
278	230	21672	27.3	24.2	24.2	6.1	33
278	230	29991	21.4	14.3	14.3	0.0	28
279	239	18804	72.7	66.7	57.6	0.0	33
280	238	23984	54.5	45.5	39.4	3.0	33
280	238	24496	39.4	36.4	30.3	0.0	33
280	238	32815	50.0	42.9	25.0	0.0	28
281	228	18240	54.5	39.4	9.1	0.0	33
282	235	20196	33.3	24.2	15.2	0.0	33
283	237	18100	24.2	9.1	3.0	0.0	33
284	241	17398	42.4	27.3	12.1	12.1	33
285	242	18102	60.6	45.5	0.0	0.0	33
286	243	17386	57.6	42.4	3.0	0.0	33
287	258	18886	33.3	18.2	3.0	0.0	33
288	261	18904	45.5	36.4	15.2	6.1	33
289	260	19590	24.2	6.1	0.0	0.0	33
290	236	18801	45.5	33.3	0.0	0.0	28
293	246	18089	54.5	36.4	6.1	0.0	33
294	245	17385	51.5	39.4	12.1	0.0	33
295	248	19603	48.5	21.2	9.1	0.0	33
296	129	18552	57.6	42.4	18.2	0.0	33
298	2	19950	63.6	54.5	36.4	3.0	33
299	254	19264	24.2	12.1	9.1	0.0	33
300	249	17836	48.5	39.4	9.1	0.0	33
301	2	19604	36.4	36.4	21.2	3.0	33
302	224	18445	39.4	24.2	6.1	0.0	33
303	222	17035	33.3	27.3	15.2	0.0	28
304	208	19600	45.5	33.3	3.0	0.0	33
305	250	18903	57.6	39.4	9.1	0.0	33
306	251	21017	57.6	33.3	6.1	0.0	33
307	252	20315	72.7	57.6	9.1	0.0	33
308	253	20303	30.3	6.1	3.0	0.0	33
309	257	22775	57.6	39.4	12.1	0.0	33

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
1	2.761	1.000	2.624	1.389	3.424
2	1.000	1.000	1.557	1.000	1.661
2	1.716	1.000	1.560	2.388	1.956
3	2.761	1.000	2.624	1.389	3.424
4	1.000	1.000	7.846	1.000	0.617
5	2.116	0.651	1.000	7.186	3.771
6	2.426	3.697	1.824	2.357	1.716
7	2.026	2.571	2.649	1.557	2.131
9	1000.000	1.000	3.101	1.782	4.160
10	2.993	1.000	3.340	3.892	2.465
11	1.000	1.000	5.076	4.513	3.318
12	1000.000	1000.000	7.265	6.431	2.414
13	1.000	1.000	2.347	1.000	4.672
14	1.000	1.000	2.285	1.286	1.974
15	1000.000	1.000	3.286	1.810	2.354
16	1000.000	1.000	2.864	1.000	1.259
17	1000.000	1000.000	1.655	6.303	3.397
18	1000.000	1.000	1.770	1.712	2.754
19	1.556	2.224	1.000	3.926	2.670
20	1.000	1000.000	2.477	1.874	2.279
21	2.789	1.000	3.077	1.555	1.990
22	1000.000	1.000	1.990	1.948	10.871
23	1000.000	1.000	1.997	1.499	2.115
24	2.208	1.000	2.375	1.338	1.722
25	1000.000	1.000	2.104	1.000	3.357
26	1.000	1.000	3.618	1.418	1.865
27	1.427	1.756	2.055	1.433	1.329
28	1000.000	1.000	2.701	1.498	5.087
29	1000.000	1.000	2.618	2.398	2.494
30	1000.000	1.000	1.000	1000.000	1.000
31	6.078	1.000	1.000	1.676	2.671
32	1.692	5.174	8.415	3.037	2.533
33	1.804	1.000	2.969	1.000	1.000
34	1000.000	1000.000	1.921	1.211	1.218
35	1.000	1.000	1.000	1000.000	2.909
36	1000.000	1.000	2.295	1.244	1.192
37	1000.000	2.566	4.346	1.483	1.527
38	2.929	1.975	2.398	1.950	2.432
39	1.000	1.000	2.625	1.000	2.319

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
40	1000.000	1.000	1.948	1.000	1.723
41	1.000	1.000	1.000	2.650	4.380
42	1.000	2.076	2.176	1.510	2.006
43	1.000	1.000	1.941	1.504	2.506
44	1.000	1.000	2.940	1.338	1.972
45	1.892	0.726	2.936	5.154	1.979
46	1.183	1.000	3.099	1.905	1.802
47	1.000	1.000	2.552	1.788	1.712
48	1.000	3.033	1.876	1.534	3.224
49	1.000	1.000	1.924	2.248	2.115
50	1.000	0.694	1000.000	1000.000	2.033
51	1000.000	1.000	1000.000	1000.000	10.350
52	1000.000	1.000	2.628	1.482	1.513
53	1.000	1.000	2.382	1.527	2.852
54	1.000	1.000	2.744	1.000	2.582
56	1.000	0.001	1000.000	1000.000	3.771
57	1.000	1.000	1000.000	1000.000	1.000
58	1.000	1.000	3.499	3.027	2.123
59	2.224	1.593	18.923	7.326	9.036
60	1.543	1.540	1.920	1.682	2.048
61	1000.000	5.003	2.042	1.397	2.111
62	1000.000	5.233	5.721	2.741	1.479
63	1000.000	1.000	18.741	2.395	22.642
64	1000.000	1.000	1.196	1000.000	2.800
65	1.000	1.000	2.268	1.000	3.249
66	1000.000	3.893	1.868	1.522	2.851
67	1000.000	1.000	2.835	1.846	2.489
68	1000.000	1.000	2.525	1.759	2.169
70	1000.000	1.000	1.596	1.266	1.663
71	1.838	4.633	1.693	1.499	1.993
73	2.237	1000.000	1.698	1.611	2.902
74	4.085	8.145	4.003	3.670	3.347
75	1.957	1000.000	1.000	1000.000	3.706
76	3.116	4.674	10.908	1.757	4.006
77	1.000	1.000	6.514	4.795	4.644
78	1.000	3.002	2.275	1.362	2.775
79	1000.000	1.000	2.166	1.599	4.851
80	5.677	20.269	0.863	5.930	5.335
81	1000.000	1.174	2.105	1.432	1.858
82	1.000	1.799	2.415	1.631	3.011

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
83	1.000	1.000	6.041	0.648	1.248
84	1.754	2.406	1.581	1.630	2.324
85	3.699	1.000	2.572	2.706	4.058
86	1.810	1.000	2.645	2.668	3.011
87	2.412	1.000	1.000	1.855	2.067
88	1.940	1000.000	3.267	2.591	2.478
89	1.588	1.000	3.774	1.000	2.082
90	4.063	1.000	3.050	1.641	2.236
91	1.000	1.000	2.366	2.076	3.538
92	2.442	2.721	2.040	2.023	1.718
93	1.869	2.656	1.981	1.867	2.976
94	1.578	2.570	3.147	3.108	1.409
95	1.000	1.000	1.000	1000.000	2.639
96	2.511	2.014	3.034	1.000	3.949
97	1.763	1.000	2.995	2.346	2.966
98	2.860	1000.000	11.375	1.000	3.160
99	1.544	1000.000	2.332	1.185	1.499
100	1.936	4.870	2.352	2.657	2.798
101	1.000	1.000	2.993	1.627	3.124
102	1.334	1000.000	1.794	1.118	1.393
104	1.000	1000.000	3.748	1.434	5.918
106	2.295	3.123	2.483	3.612	2.496
107	1.799	1.000	3.077	2.443	2.034
108	1.503	1.000	2.081	1.659	2.219
109	2.151	1.000	2.351	3.804	2.446
110	1000.000	2.518	1.981	1.000	1.257
111	7.031	0.001	1.000	1.000	6.786
112	1.836	3.648	2.918	2.181	2.574
113	3.566	1.000	3.022	4.886	1.000
114	2.006	1.000	1.780	1.751	1.881
116	2.237	1000.000	1.698	1.611	2.902
118	1.000	1.000	1.557	1.000	1.661
118	1.716	1.000	1.560	2.388	1.956
119	1000.000	1.000	2.175	1.000	3.588
120	2.732	3.756	3.601	2.818	1.423
121	1000.000	1.000	1.000	1.000	3.160
122	1000.000	0.631	1.000	9.124	5.154
123	9.353	1.000	9.041	1000.000	60.900
124	9.353	1.000	9.041	1000.000	60.900
125	1.308	1000.000	8.239	1.000	8.873

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
126	1.308	1000.000	8.239	1.000	8.873
130	2.926	1.000	15.441	1.000	1.859
131	1.957	1000.000	1.000	1000.000	3.706
132	1.578	2.570	3.147	3.108	1.409
133	1.578	2.570	3.147	3.108	1.409
134	1.957	1000.000	1.000	1000.000	3.706
135	1.879	1000.000	3.193	1.000	4.631
136	1.869	2.656	1.981	1.867	2.976
138	1.000	1.000	1.557	1.000	1.661
138	1.716	1.000	1.560	2.388	1.956
140	1.739	1.000	2.192	2.207	1.473
141	2.450	1000.000	6.871	3.305	5.197
142	2.412	1.000	1.000	1.855	2.067
143	2.412	1.000	1.000	1.855	2.067
144	4.063	1.000	3.050	1.641	2.236
145	1.000	1.000	3.211	2.729	3.010
147	2.119	2.693	1.000	2.263	2.473
148	1.556	2.224	1.000	3.926	2.670
149	2.164	0.727	1.000	2.791	0.742
150	3.331	2.910	1.000	2.067	3.095
151	6.078	1.000	1.000	1.676	2.671
152	4.070	7.471	1.000	2.847	3.918
152	1.000	1.000	1.000	1000.000	1.000
153	4.070	7.471	1.000	2.847	3.918
153	1.000	1.000	1.000	1000.000	1.000
154	2.176	3.237	1.000	2.133	1.944
155	3.864	2.116	1.000	1.870	2.818
156	2.134	3.008	1.000	1.960	2.466
157	2.723	1.322	0.486	1.689	3.517
159	3.720	6.801	2.345	1.402	3.668
161	2.770	2.866	1.000	1.191	3.059
162	2.257	1000.000	0.626	1000.000	1.000
163	2.467	3.639	1.720	2.287	1.894
164	1.711	1.000	1.000	1.504	1.147
165	0.437	1.000	1.000	2.678	7.488
166	4.907	1.000	1.000	1.209	3.192
168	3.380	1.583	1.000	1.623	3.075
169	3.647	4.679	1.000	2.314	3.294
170	3.403	1.000	1.000	1.184	2.741
171	1.700	5.306	1.000	2.102	1.000

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
171	2.473	3.169	0.627	1.895	1.263
172	1.700	5.306	1.000	2.102	1.000
172	2.473	3.169	0.627	1.895	1.263
173	1.000	1.000	1.000	2.805	1.737
174	2.588	3.048	1.000	1.624	2.734
176	2.025	1.000	1.000	1.673	1.000
177	3.039	1.000	1.773	1.722	2.704
179	2.446	1.920	1.000	1.423	1.000
180	3.096	1.596	1.000	1.572	5.294
181	3.179	9.201	1.000	1.963	3.506
182	2.824	1.000	1.000	1.233	1.976
183	1.620	3.925	0.694	2.020	1.592
184	2.206	1.000	1000.000	3.501	2.543
185	2.206	1.000	1000.000	3.501	2.543
190	1.234	3.022	1.000	1.869	1.999
191	1.234	3.022	1.000	1.869	1.999
192	4.102	4.304	1.000	2.271	2.467
193	3.560	4.060	1.000	2.230	2.297
194	1.000	3.758	1.000	11.805	9.755
198	1.267	2.776	1.000	1.919	1.935
200	2.004	3.190	1.000	2.435	1.313
201	2.776	2.529	1.000	1.924	2.382
202	2.245	2.831	0.455	2.905	2.739
204	1.906	2.710	1.000	2.913	1.783
205	1.906	2.710	1.000	2.913	1.783
206	2.106	2.362	1.000	2.460	1.776
207	2.393	1.865	1.000	2.021	1.865
208	3.802	2.020	1.000	2.226	2.202
209	2.581	2.351	1.000	1.791	2.155
209	1.000	1.346	1.000	1.000	1.277
210	3.706	6.720	1.000	2.481	3.263
211	1.948	2.903	1.000	1.599	1.930
212	11.732	1.000	1.000	3.443	3.059
213	1.437	1.807	1.000	3.076	2.488
214	1.493	1.000	1.000	1.000	1.000
215	1.605	2.244	1.000	2.300	1.000
217	2.825	1.000	1.000	1.306	1.926
218	2.855	6.659	1.000	2.594	2.835
220	1.000	1.000	1.000	1.278	2.456
222	2.490	1.000	2.411	1.527	2.166

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
223	1.595	2.786	2.219	2.254	2.476
224	5.732	2.587	2.103	2.577	2.360
225	2.911	2.883	3.991	1.852	2.229
226	1.000	1.000	2.651	2.283	1.304
227	1.661	2.315	8.377	1.513	2.070
228	2.926	1.000	15.441	1.000	1.859
230	2.714	5.093	1.000	21.125	1.909
231	3.791	2.443	0.805	3.728	2.623
232	2.843	3.250	1.000	2.467	1.800
233	1.435	2.783	1.000	1.471	1.630
234	1.810	1.000	1.640	2.521	1.929
235	2.047	1.000	6.181	6.095	1.660
236	2.391	1.791	2.109	3.120	1.822
239	1.000	1.000	1.000	1000.000	5.199
240	1.000	1.000	1.452	1000.000	1.560
242	1000.000	1.000	1000.000	1.000	1.000
243	2.583	4.225	1.000	1.000	2.480
247	2.464	1.861	0.217	1.711	3.396
248	1.000	1000.000	1.000	1.000	1000.000
249	1000.000	1000.000	1.000	1.543	3.438
250	1.760	1000.000	1.000	1.000	3.216
252	1.677	3.031	3.547	3.698	2.478
253	1000.000	1.000	1000.000	1.000	1.000
254	2.419	1.380	1.000	1.716	2.407
255	1000.000	1.000	1.989	1000.000	1.000
256	1.000	1.000	1.000	1.679	1.483
257	1000.000	1.000	2.492	1.000	6.169
258	1.000	1.000	2.057	1000.000	2.923
260	1.000	1.000	2.988	2.849	4.139
262	2.847	3.114	1.000	0.721	2.023
263	2.091	6.136	1.000	1.807	3.344
264	3.343	3.831	1.000	2.595	3.008
265	2.523	5.144	0.589	1.871	3.449
266	1.639	5.315	0.126	1.606	2.531
267	2.211	3.455	1.000	3.444	2.298
268	1.000	1.000	1.000	1.260	5.554
269	1.000	1.000	1.000	1.216	9.792
270	1.433	6.280	1.000	1.571	2.366
271	2.397	3.229	1.000	2.662	1.304
272	1.000	1.000	1.000	1000.000	2.779

Table6
Microarray Data

SEQ ID NO	15Ratio	52Ratio	121Ratio	125Ratio	128Ratio
273	3.069	2.168	1.000	2.343	1.000
273	3.724	1.000	1.445	2.374	1.840
273		2.316	1.833	2.330	2.025
274	2.257	2.857	1.000	2.426	1.726
274	2.281	2.886	1.000	2.562	1.531
274		4.366	1.638	2.524	1.422
275	2.894	2.159	1.000	2.511	1.988
275	2.686	1.959	1.000	2.519	1.919
275		3.025	1.894	2.057	1.907
276	4.159	6.846	1.000	6.258	4.256
277	2.785	2.269	1.000	2.790	2.110
277	2.648	2.289	1.738	2.996	1.977
277		3.757	1.791	2.647	1.854
278	1.000	1.000	1.000	1.000	1.000
278	1.000	1.000	1.000	1.000	1000.000
278		1.000	1.000	1.000	1000.000
279	1000.000	1.000	10.576	16.110	13.087
280	1000.000	1.000	2.434	1.365	1.000
280	1000.000	1.000	1.000	1.000	1.000
280		1.000	2.934	1.238	3.709
281	2.033	1.000	2.780	1.809	2.447
282	1.000	1.000	2.004	1.605	1.878
283	1.225	1.000	1.412	1.692	1.717
284	2.761	0.769	1.000	2.724	5.667
285	1.305	1.000	2.900	1.563	1.888
286	2.158	1.000	3.241	2.575	1.449
287	1.000	1.000	1.446	1.369	1.510
288	1.000	1.000	1.968	1.000	3.154
289	1.369	1.000	1.317	1.356	2.511
290	1.000	1.000	2.272	1.409	4.133
293	2.077	1.539	2.889	1.591	2.206
294	2.940	1.907	1.802	3.148	1.565
295	2.304	1.000	2.475	1.840	1.283
296	1.000	1.000	3.032	1.553	2.854
298	1000.000	0.672	1.000	9.151	4.600
299	1.000	1.000	2.459	1.323	1.842
300	1.000	1.000	2.835	1.798	2.684
301	1.000	0.659	1.000	1.000	4.645
302	2.783	1.000	1.536	1.891	1.000
303	1.000	1.000	1.239	1.000	2.064
304	1.735	1.000	1.454	2.021	1.907
305	3.022	1.794	1.945	2.529	1.839
306	1.000	1.000	1.630	2.277	1.728
307	1.648	2.020	3.389	2.120	3.863
308	1.000	1.000	1.783	2.326	2.284
309	1.484	3.928	1.000	2.503	2.298

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
1	1.000	1.000	1.429	3.377	2.236	3.294
2	2.544	1.000	1.686	5.093	1.000	1000.000
2	2.540	1.000	2.135	3.765	1.523	3.032
3	1.000	1.000	1.429	3.377	2.236	3.294
4	0.788	0.001	0.811	1.563	1.000	5.434
5	1.487	2.053	1.679	0.553	2.095	14.637
6	1.627	3.348	2.258	2.473	1.652	2.633
7	1.853	4.642	2.150	1.415	1.869	3.326
9	2.152	1.000	1.000	2.173	1000.000	4.993
10	3.378	3.081	4.194	2.541	1.000	4.697
11	3.038	3.091	1.000	0.688	1.000	6.596
12	1.000	4.924	2.723	11.253	1.000	1000.000
13	1.000	1.000	1.000	1.381	1.000	3.933
14	1.679	1.989	1.586	2.182	1.555	2.720
15	2.293	3.549	1.000	1.901	1000.000	3.651
16	1.000	1.703	1.000	1.000	1.000	1.686
17	6.509	14.088	1.000	2.287	5.974	1000.000
18	1.000	4.468	2.388	3.839	1000.000	2.440
19	3.078	2.076	1.428	1.000	1.836	1000.000
20	1.000	2.552	1.232	1.698	2.558	3.128
21	1.792	2.361	1.904	1.670	2.031	2.869
22	4.983	8.514	15.606	0.356	2.560	6.236
23	1.000	1.000	1.000	2.123	1000.000	1000.000
24	1.670	1.863	1.000	1.690	1.000	1000.000
25	1.000	1.000	2.410	1.183	1.315	1000.000
26	1.000	2.597	0.725	2.162	1.000	2.594
27	1.000	1.762	1.455	1.000	1.446	3.851
28	2.327	1.000	3.440	1.281	1000.000	1.277
29	1.687	1.000	1.819	13.707	1000.000	1000.000
30	1.546	0.001	1.000	1.000	1.000	1.000
31	2.849	2.956	1.299	1.533	2.400	2.015
32	2.447	2.391	1.000	2.699	4.607	1.719
33	1.000	1.979	0.477	2.810	1.899	2.346
34	1.000	1.812	3.290	1.351	1000.000	1000.000
35	1.000	0.001	1.000	2.767	1.000	1.660
36	1.621	2.052	1.000	4.754	1.000	1.000
37	1.000	1.000	1.000	2.702	2.732	2.128
38	2.087	2.901	1.420	2.963	1.943	4.468
39	1.000	1.637	1.000	1.594	2.069	1.730

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
40	1.000	2.324	1.328	1.457	1.000	1.000
41	1000.000	1.000	1.000	3.401	1000.000	1000.000
42	1.908	3.057	2.884	0.742	2.648	3.773
43	1.435	2.943	1.917	1.227	1.429	2.614
44	2.105	2.199	1.138	1.000	1.000	1.485
45	2.623	3.586	4.350	2.500	3.791	5.252
46	1.353	2.214	1.273	2.522	1.510	3.882
47	1.939	2.745	1.924	4.446	1.000	1.521
48	1.523	2.479	1.452	1.896	2.162	2.169
49	1.000	2.064	1.000	1.570	1.438	3.874
50	1.881	1.000	0.001	1.000	1.000	1.000
51	1.000	1.000	1.000	2.457	1.000	1.000
52	1.457	1.000	2.905	1.673	1.000	1.000
53	3.921	0.495	1.000	1.000	1.000	2.573
54	1.000	1.579	1.000	0.693	1.000	2.195
56	1000.000	1.000	1.000	2.300	1.000	3.770
57	1000.000	1.000	1.000	1.000	1.000	7.142
58	1.444	2.871	1.000	7.616	1.905	3.054
59	4.480	8.610	1.870	1.000	5.750	4.862
60	1.000	1.711	1.704	2.038	1.455	1.858
61	1.212	2.834	1.000	4.669	2.330	2.088
62	1.873	1.000	3.530	2.462	1000.000	9.274
63	9.481	27.153	7.785	0.190	1000.000	11.599
64	2.900	1.000	1.000	1.000	1.000	1000.000
65	0.894	3.198	4.913	8.159	1000.000	1.262
66	1.706	2.329	3.495	1.650	1.540	1000.000
67	1.544	4.295	1.562	1.841	1000.000	1000.000
68	1.000	2.108	1.000	2.754	1000.000	3.071
70	1.407	1.697	1.869	2.276	1.673	3.521
71	2.055	2.648	1.110	2.128	0.790	2.703
73	1.362	3.787	1.655	4.649	1.565	2.084
74	2.451	6.004	3.289	3.166	2.722	5.203
75	1000.000	1.000	1.000	1.000	1.639	1000.000
76	0.623	5.526	1.813	2.551	1.696	7.856
77	1.000	3.598	1.878	3.092	2.409	8.008
78	2.390	2.945	1.814	1.228	1.199	4.500
79	1.000	1.000	1.000	2.438	1000.000	1000.000
80	6.144	14.118	1.292	1.843	4.376	10.898
81	1000.000	2.328	1.264	3.330	1.000	1000.000
82	1.959	3.316	2.405	2.138	1.633	2.273

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
83	1.492	2.310	2.213	1.736	1.000	1.000
84	1.680	2.665	1.819	2.387	1.196	2.856
85	3.017	3.241	2.897	2.901	2.076	3.591
86	2.965	3.272	3.000	2.313	1.999	4.204
87	1.000	2.005	4.007	1.928	2.515	5.009
88	1.462	1.000	1.643	2.991	2.238	2.519
89	2.377	3.757	5.550	2.830	4.034	5.750
90	1.984	1.000	1.661	3.401	1.541	4.619
91	2.076	2.880	1.371	1.441	1.526	2.306
92	1.667	2.678	2.882	2.171	1.934	6.269
93	1.000	1.757	2.180	1.960	3.788	2.095
94	1.675	3.316	3.317	2.132	1.282	3.061
95	2.042	1.000	1.000	3.004	1.000	1.000
96	1.663	3.013	1.563	1.433	1.348	2.900
97	3.408	3.089	1.361	2.333	1.490	2.800
98	3.947	6.370	1.765	0.001	1.647	4.604
99	1.323	1.000	1.942	3.166	1.872	3.729
100	1.940	2.685	2.810	1.280	2.031	4.468
101	1.795	2.752	2.260	1.680	1.922	2.413
102	1.392	1.000	1.604	1.000	1.000	1.892
104	2.630	1.000	4.726	1.000	1.997	1.681
106	3.862	4.606	1.843	1.585	1.143	1.862
107	1.213	2.008	3.856	1.000	1.426	3.677
108	2.225	2.454	1.692	2.504	2.310	2.431
109	2.767	3.698	1.628	1.000	1.000	2.981
110	1.538	1.000	1.564	1.373	1.000	2.849
111	1.000	1000.000	10.954	1.000	1.000	1000.000
112	2.881	2.458	1.463	2.427	1.523	2.859
113	4.079	0.001	1.436	3.804	1.000	4.038
114	2.190	2.055	2.167	2.662	1.820	2.075
116	1.362	3.787	1.655	4.649	1.565	2.084
118	2.544	1.000	1.686	5.093	1.000	1000.000
118	2.540	1.000	2.135	3.765	1.523	3.032
119	1.000	0.001	1.000	1.000	2.379	1.000
120	1.742	5.457	2.449	2.244	2.083	4.360
121	1.000	1.000	1.000	1.000	1.000	1000.000
122	3.238	1.000	1.000	9.006	1.000	8.214
123	1.000	12.731	18.877	1.000	2.996	7.638
124	1.000	12.731	18.877	1.000	2.996	7.638
125	1.000	7.033	2.749	0.669	7.983	1000.000

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
126	1.000	7.033	2.749	0.669	7.983	1000.000
130	1.966	3.506	4.974	0.001	1.000	12.772
131	1000.000	1.000	1.000	1.000	1.639	1000.000
132	1.675	3.316	3.317	2.132	1.282	3.061
133	1.675	3.316	3.317	2.132	1.282	3.061
134	1000.000	1.000	1.000	1.000	1.639	1000.000
135	1000.000	1000.000	1.000	1.000	1.000	1000.000
136	1.000	1.757	2.180	1.960	3.788	2.095
138	2.544	1.000	1.686	5.093	1.000	1000.000
138	2.540	1.000	2.135	3.765	1.523	3.032
140	1.000	1000.000	1.837	1.000	1.000	3.119
141	1000.000	1.000	1.000	0.001	1.000	1000.000
142	1.000	2.005	4.007	1.928	2.515	5.009
143	1.000	2.005	4.007	1.928	2.515	5.009
144	1.984	1.000	1.661	3.401	1.541	4.619
145	3.241	3.484	2.140	13.434	3.851	2.839
147	1.000	3.656	2.278	1.651	1.788	1.000
148	3.078	2.076	1.428	1.000	1.836	1000.000
149	1.443	0.608	2.475	1.737	1.311	1.000
150	1.564	1.906	1.497	2.071	1.933	2.023
151	2.849	2.956	1.299	1.533	2.400	2.015
152	2.652	5.356	2.301	1.635	2.784	6.307
152	1.000	1.765	1.000	0.511	1.000	1.000
153	2.652	5.356	2.301	1.635	2.784	6.307
153	1.000	1.765	1.000	0.511	1.000	1.000
154	2.101	2.449	1.957	1.825	1.281	1.885
155	2.618	3.034	1.276	1.000	1.934	2.010
156	2.040	1.828	1.519	2.141	1.659	2.141
157	1.610	1.945	1.000	1.134	1.617	2.427
159	2.553	3.098	3.340	2.328	4.852	2.176
161	1.397	1.693	1.634	3.235	1.401	1.489
162	1000.000	1.508	1.000	1.000	2.550	1000.000
163	2.150	2.684	2.447	2.227	1.281	1.901
164	2.177	3.926	2.898	0.774	1.659	1.622
165	1.950	2.988	0.574	0.246	1.000	7.171
166	1.984	2.133	1.287	1.178	0.877	4.871
168	1.899	2.953	1.341	1.605	1.846	1.423
169	2.018	2.918	2.275	2.724	2.796	2.700
170	1.736	2.025	1.571	0.797	1.638	1.492
171	1.582	3.400	1.122	3.825	1.676	2.180

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
171	1.581	2.376	1.192	2.002	1.660	1.870
172	1.582	3.400	1.122	3.825	1.676	2.180
172	1.581	2.376	1.192	2.002	1.660	1.870
173	1.000	2.990	1.000	1.677	1.407	1000.000
174	1.560	4.095	1.671	1.680	2.326	3.014
176	1.000	2.526	1.000	1.520	1.635	2.392
177	1.622	4.544	1.447	1.227	2.393	1000.000
179	1.791	1.854	1.344	1.114	1.634	1.000
180	3.055	5.187	1.945	1.152	1.817	3.466
181	2.201	6.653	1.427	1.732	3.406	1.000
182	1.639	2.218	2.383	1.000	2.526	1.743
183	2.062	2.682	1.000	0.829	1.000	2.461
184	1.000	3.191	1.000	0.824	1.307	1000.000
185	1.000	3.191	1.000	0.824	1.307	1000.000
190	1.625	3.551	1.218	1.966	1.398	1.785
191	1.625	3.551	1.218	1.966	1.398	1.785
192	2.402	4.519	3.700	2.133	1.605	5.974
193	2.443	4.140	3.351	2.001	1.580	5.819
194	7.661	9.286	4.400	1.000	8.053	8.246
198	1.549	3.664	1.421	2.054	1.476	1.707
200	1.782	3.214	1.388	1.327	1.580	2.738
201	2.006	2.440	2.495	1.478	1.939	5.082
202	2.854	3.895	1.705	1.496	2.282	3.051
204	2.273	2.891	1.770	1.360	1.542	2.271
205	2.273	2.891	1.770	1.360	1.542	2.271
206	1.936	2.187	1.826	1.268	1.321	1.987
207	2.365	3.644	1.776	1.343	1.838	2.854
208	1.803	2.572	1.000	2.870	2.293	2.949
209	2.318	2.922	1.371	2.802	1.166	3.280
209	1.000	1.000	1.000	0.813	1.000	1000.000
210	2.413	5.285	1.669	1.000	2.764	5.021
211	1.721	3.610	1.217	2.152	1.235	2.242
212	1.851	4.779	0.703	0.049	2.534	6.614
213	3.323	2.277	2.241	1.181	1.442	3.297
214	1000.000	0.001	1.213	0.001	1.000	1000.000
215	2.765	3.920	1.339	1.513	1.220	1000.000
217	1.000	1.698	1.905	1.495	1.403	1000.000
218	1.000	4.368	1.698	1.000	3.079	3.626
220	1.000	1.945	1.711	1.909	1.000	1000.000
222	1.903	3.616	1.766	1.808	1.865	2.873

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
223	2.404	1.000	3.025	3.418	1.431	3.140
224	2.327	4.955	2.156	1.610	3.101	7.771
225	1.747	3.722	2.612	1.756	4.298	5.998
226	1.000	1.612	1.909	7.917	1.744	4.277
227	1.000	1.000	1.880	1.936	1.970	3.271
228	1.966	3.506	4.974	0.001	1.000	12.772
230	1.000	15.931	1.821	3.498	1.515	1.000
231	2.131	3.009	1.000	2.072	1.438	1000.000
232	1.645	3.053	1.418	2.847	1.395	2.388
233	1.000	2.065	1.000	1.479	1.435	1.000
234	2.034	3.632	2.045	1.892	1.604	2.459
235	1.731	2.491	2.095	0.496	1.132	4.777
236	1.411	3.257	1.619	2.045	1.000	1.399
239	2.578	1.558	1.358	1.000	1.000	1.441
240	0.760	1.000	1.965	1.839	1.000	1.558
242	1000.000	1.000	0.001	1.000	1.000	1.000
243	1.552	3.091	1.630	2.725	1.616	1000.000
247	1.621	2.002	1.462	1.805	1.431	1.000
248	1000.000	1.000	1.000	0.001	1.000	1000.000
249	1.000	3.915	1.000	3.225	1.863	1000.000
250	1.000	2.658	1.000	2.295	1.214	1000.000
252	1.000	2.310	1.000	5.133	4.021	5.077
253	1.000	1.000	1.000	1.000	1.000	1.743
254	1.746	2.805	2.021	2.771	1.501	1.766
255	2.080	1.000	1.000	1.000	1.000	1.000
256	1.000	2.661	1000.000	1.924	1.198	1000.000
257	2.828	1.000	2.602	1.788	1.000	2.058
258	1.000	1.335	1.600	1.443	1.000	1.774
260	1.304	5.125	1.000	1.130	1.456	2.152
262	1.741	3.114	2.585	2.647	2.110	1000.000
263	2.904	3.778	3.972	1.655	1.716	5.008
264	3.599	4.621	1.400	4.206	1.860	2.264
265	2.602	3.458	2.502	4.867	2.344	3.323
266	2.344	2.427	1.823	2.767	2.942	1.615
267	2.523	4.524	1.355	2.052	1.000	2.392
268	1.714	9.819	1.000	1.426	4.010	2.265
269	1.000	18.283	1.000	0.317	1.000	1.000
270	1.986	2.155	1.600	2.556	2.499	1.620
271	1.591	3.364	2.078	2.023	1.998	3.141
272	1.000	0.001	1.000	2.997	1.000	2.012

Table6
Microarray Data

SEQ ID NO	130Ratio	133Ratio	141Ratio	156Ratio	228Ratio	264Ratio
273	1.672	3.628	2.762	0.001	1.350	1000.000
273	1.770	3.262	2.596	0.001	1.407	1000.000
273	1.000	1.000	2.089	1.533	1.394	2.029
274	1000.000	3.549	1.802	2.477	1.266	1.000
274	2.139	3.602	1.632	2.626	1.210	2.957
274	2.100	3.475	1.940	2.479	1.283	3.049
275	1.832	3.601	2.098	0.001	1.381	1000.000
275	1.820	3.618	2.080	0.001	1.386	1000.000
275	1.511	3.610	1.969	1.000	1.000	2.335
276	5.135	11.304	1.000	2.036	4.115	9.071
277	2.243	3.876	2.354	1.444	1.274	1000.000
277	2.110	4.037	2.289	1.703	1.254	1000.000
277	1.953	1.000	2.789	1.000	1.000	2.189
278	1.000	1.000	1000.000	0.001	1.127	1000.000
278	1.886	1.000	1000.000	0.001	1.000	1000.000
278	1000.000	1.000	1.000	1.000	1.000	1.000
279	5.104	12.547	2.771	0.727	2.193	20.187
280	1.000	0.001	1000.000	1.000	2.326	1000.000
280	1.000	1.000	1.000	1.219	2.864	1000.000
280	1000.000	1.000	12.387	1000.000	1.000	1.629
281	1.943	4.191	1.248	1.181	2.657	1.995
282	1.505	1.000	1.000	1.450	1.000	2.359
283	1.908	2.459	1.621	1.385	1.175	1.791
284	2.054	4.533	0.770	0.297	1.279	5.163
285	2.096	3.974	1.537	2.326	1.516	3.033
286	1.592	4.143	1.737	1.926	1.496	3.052
287	1.619	1.506	1.549	2.733	1.446	2.009
288	1.943	2.526	4.717	1.796	1.000	1.000
289	1.774	1.935	1.209	2.757	1.429	2.092
290	1.635	2.668	1.996	1.743	1.000	3.266
293	2.507	2.605	1.847	1.701	1.356	2.282
294	1.640	2.902	1.632	2.885	1.508	2.748
295	1.000	2.004	1.521	2.283	1.283	1.588
296	1.664	5.364	1.604	1.742	1.502	1.730
298	1.762	2.739	2.103	0.369	3.002	15.773
299	1.499	1.297	1.943	1.348	2.244	1.000
300	1.711	2.845	2.263	4.123	1.000	2.073
301	1.000	3.064	1.850	0.279	1.000	1.000
302	1.519	3.551	1.000	1.882	1.473	2.704
303	3.539	2.516	1.000	1.000	1.000	1.869
304	1.992	4.449	1.318	1.785	1.000	1.936
305	1.571	3.718	2.599	2.066	1.604	1.632
306	2.113	3.200	1.893	1.970	1.000	2.551
307	2.875	4.217	3.439	1.537	1.615	4.726
308	1.000	2.220	1.259	1.708	1.207	1.267
309	2.476	5.588	1.661	1.872	1.000	1.917

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
1	3.272	1.968	4.441	1.000	1.000	3.875
2	3.334	1.000	1.000	1000.000	1.000	1.000
2	3.053	2.254	4.769	1000.000	1.000	1.000
3	3.272	1.968	4.441	1.000	1.000	3.875
4	1.370	1.000	1.468	1.000	1.000	1.000
5	8.639	2.928	1.000	3.898	1.187	5.625
6	2.686	1.305	1.947	1.000	1.335	1.000
7	2.580	3.265	3.597	8.428	1.361	4.165
9	1000.000	2.520	1.000	1.000	1.000	1000.000
10	2.822	6.319	10.583	11.493	4.251	8.928
11	7.631	3.511	5.653	1.000	1.210	4.403
12	15.710	4.125	4.349	1.000	3.051	1.000
13	3.154	1000.000	2.768	1.000	1.000	9.650
14	2.018	3.426	2.045	4.418	1.000	1.587
15	2.061	3.286	2.048	1000.000	1.000	4.276
16	1.559	1.822	1.652	4.374	2.427	3.542
17	14.013	8.787	12.730	1000.000	2.781	1.000
18	2.131	3.103	2.234	1000.000	1.498	1000.000
19	1.225	2.191	3.674	1.000	3.113	1.000
20	3.682	3.964	2.868	1.000	1.373	1000.000
21	1.712	3.639	3.528	1.000	1.607	2.698
22	9.443	1.819	4.388	1000.000	10.522	1000.000
23	1000.000	2.014	1.560	1000.000	1.000	1000.000
24	1.591	2.726	2.946	1.000	1.354	1000.000
25	1000.000	1.906	3.428	1000.000	1.314	1.000
26	2.833	2.173	3.013	1000.000	1.000	1.000
27	2.186	2.192	2.095	1.927	1.630	2.039
28	1.554	1.920	1.323	1.000	1.000	1000.000
29	3.125	2.664	2.640	1.000	1.000	1000.000
30	1.000	1000.000	1.000	1.000	1.000	1.000
31	1.860	1000.000	2.219	1.000	1.589	1.000
32	8.277	5.861	7.163	7.274	3.124	2.056
33	2.119	1.986	3.573	1.376	0.915	1.000
34	1.544	2.326	1.972	1.000	1.000	1.000
35	1.000	1000.000	0.001	1.000	1.000	2.032
36	2.071	1.790	1.277	1.000	0.611	1000.000
37	3.516	1.000	4.254	1.000	1.000	1.000
38	4.094	2.952	2.084	5.182	1.251	1.000
39	2.442	1000.000	0.001	1.000	1.449	2.995

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
40	1.690	3.187	1.720	3.979	1.000	1.000
41	1.000	1000.000	1.000	1000.000	1.000	1.000
42	3.140	1.860	2.373	1.000	2.461	1.000
43	2.164	2.717	2.875	1000.000	1.093	3.550
44	2.358	3.048	2.244	1.000	1.351	4.577
45	4.154	3.831	4.075	1.000	2.985	7.932
46	1.980	2.204	2.701	1.000	1.121	3.414
47	1.843	2.186	2.622	1000.000	1.000	4.984
48	2.334	2.312	3.478	6.439	1.000	2.274
49	3.688	2.926	3.972	5.239	1.000	4.054
50	4.385	1000.000	1.000	1.000	1.371	1000.000
51	1.000	1000.000	1.000	1.000	2.553	1000.000
52	1.507	1.984	0.001	1.000	1.588	2.378
53	3.035	0.661	0.001	1.000	0.663	1.924
54	2.338	1.000	1.351	1.000	1.000	1000.000
56	3.986	1000.000	2.878	1.000	2.184	1000.000
57	1.000	1000.000	1.000	1.000	1.000	1.000
58	1.904	1.724	3.114	1000.000	0.527	3.608
59	6.502	6.505	5.486	4.924	10.074	8.792
60	1.440	3.299	2.025	2.017	1.490	2.905
61	2.135	2.483	3.246	1000.000	0.347	1.000
62	3.574	3.641	4.946	1.000	1.817	1000.000
63	36.644	29.854	37.231	1.000	1.000	1.000
64	1.000	1.000	1.000	1.000	1.000	1000.000
65	1.922	3.054	3.121	1000.000	0.001	1.000
66	2.262	3.087	2.006	1000.000	2.809	1000.000
67	2.395	2.108	2.971	1000.000	1.000	1.000
68	1.000	3.085	2.407	1.000	1.460	1000.000
70	2.539	2.088	1.769	1000.000	1.000	1.766
71	1.496	1.481	1.837	1.000	1.611	2.420
73	2.497	3.640	2.171	1.000	0.801	2.327
74	4.684	3.705	6.682	1000.000	2.067	14.380
75	1000.000	1000.000	1.000	1000.000	0.001	1.000
76	8.887	2.196	4.188	1.533	0.445	17.101
77	6.942	1000.000	6.845	1.000	2.182	1.000
78	2.718	3.255	1.840	3.579	1.000	7.015
79	1000.000	3.213	4.614	1000.000	1.000	1.000
80	10.085	5.623	11.588	24.554	7.103	1.000
81	1.540	2.861	3.128	1000.000	1.200	1000.000
82	1.696	4.047	4.601	1.000	1.794	1.000

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
83	2.032	1.658	1.902	2.762	1.446	2.030
84	2.242	2.149	2.680	4.719	1.358	3.066
85	2.236	3.471	3.858	11.092	2.320	3.448
86	1.959	4.024	6.843	11.029	2.022	1.568
87	1.000	1.000	4.575	1.000	2.441	3.222
88	2.296	1000.000	3.661	1000.000	0.681	1.000
89	4.733	3.972	3.937	6.639	3.517	6.970
90	4.014	3.557	4.689	1000.000	2.431	2.003
91	3.509	2.698	2.457	1.000	1.000	2.427
92	3.870	2.712	2.829	4.458	1.655	4.743
93	2.037	1.859	1.293	1.000	1.677	3.334
94	2.456	1.779	3.374	4.003	1.376	4.271
95	1000.000	3.904	0.001	1000.000	1.000	3.039
96	4.897	1.936	2.505	1.000	1.754	3.699
97	1.743	3.622	2.102	1.000	2.236	2.374
98	6.828	1.000	3.748	1000.000	5.268	1.000
99	4.229	2.630	3.233	1.000	1.483	3.283
100	3.064	2.574	2.898	3.818	1.569	2.540
101	1.000	3.351	3.257	2.783	1.304	5.843
102	1.861	2.571	3.922	1.000	1.149	1.000
104	1000.000	1.000	2.640	1000.000	1.256	4.406
106	2.142	3.301	3.605	6.101	2.694	3.560
107	3.347	2.558	4.110	1000.000	1.000	3.337
108	2.799	1.949	1.000	3.244	1.837	2.583
109	3.715	4.674	3.094	3.611	3.115	8.474
110	1.362	1.000	1.000	1.000	1.387	1.000
111	1000.000	1.000	1.000	1.000	0.001	1000.000
112	1.695	3.288	2.497	1.000	2.110	2.452
113	5.263	4.215	3.052	1.000	2.066	7.418
114	1.636	1.968	2.497	1.000	2.166	3.206
116	2.497	3.640	2.171	1.000	0.801	2.327
118	3.334	1.000	1.000	1000.000	1.000	1.000
118	3.053	2.254	4.769	1000.000	1.000	1.000
119	1.622	1.000	1.498	1.000	2.277	11.811
120	2.788	2.316	6.107	1000.000	1.511	6.605
121	1.000	1.000	1.000	1.000	1.000	1.000
122	3.337	1.000	1.000	1.000	1.000	1.000
123	17.754	3.972	9.350	23.562	1.520	4.495
124	17.754	3.972	9.350	23.562	1.520	4.495
125	6.626	1000.000	8.541	1.000	1.755	1.000

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
126	6.626	1000.000	8.541	1.000	1.755	1.000
130	5.066	16.154	2.388	1000.000	1.845	1.000
131	1000.000	1000.000	1.000	1000.000	0.001	1.000
132	2.456	1.779	3.374	4.003	1.376	4.271
133	2.456	1.779	3.374	4.003	1.376	4.271
134	1000.000	1000.000	1.000	1000.000	0.001	1.000
135	1.000	1000.000	1.000	1000.000	0.001	1.000
136	2.037	1.859	1.293	1.000	1.677	3.334
138	3.334	1.000	1.000	1000.000	1.000	1.000
138	3.053	2.254	4.769	1000.000	1.000	1.000
140	1.843	2.165	1.000	1.000	1.826	1.000
141	1000.000	1000.000	1.000	1.000	5.312	1.000
142	1.000	1.000	4.575	1.000	2.441	3.222
143	1.000	1.000	4.575	1.000	2.441	3.222
144	4.014	3.557	4.689	1000.000	2.431	2.003
145	3.426	3.923	2.933	1.000	1.732	3.008
147	2.178	2.148	3.522	5.642	1.564	4.393
148	1.225	2.191	3.674	1.000	3.113	1.000
149	1.000	1.266	0.717	1.501	0.842	0.550
150	1.000	1.887	1.586	1.885	1.841	3.323
151	1.860	1000.000	2.219	1.000	1.589	1.000
152	7.155	1.000	3.665	1.000	2.667	8.910
152	0.529	1.000	1.000	1.000	1.000	1.000
153	7.155	1.000	3.665	1.000	2.667	8.910
153	0.529	1.000	1.000	1.000	1.000	1.000
154	2.799	2.865	3.000	2.979	1.391	3.763
155	1.737	3.081	3.905	3.582	1.533	2.447
156	2.402	1.991	1.250	1.797	1.589	3.688
157	2.125	2.092	1.841	2.440	1.000	4.090
159	2.007	2.420	1.468	3.192	2.376	2.422
161	1.000	1.717	1.424	1.799	1.000	2.808
162	1.000	1.000	1.000	1.000	1.745	1.000
163	2.970	3.071	2.574	4.158	1.349	3.628
164	1.401	1.464	4.379	1.000	2.596	1.850
165	3.258	1.242	2.647	2.397	2.072	0.567
166	4.118	1.360	1.590	2.026	0.788	2.250
168	1.000	2.209	1.000	4.175	1.363	5.485
169	1.918	2.667	3.542	2.415	2.016	2.707
170	1.550	2.100	1.996	1.623	1.374	1.401
171	2.770	1.000	1.799	3.047	1.220	2.907

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
171	2.428	1.000	1.258	1.000	1.301	1.000
172	2.770	1.000	1.799	3.047	1.220	2.907
172	2.428	1.000	1.258	1.000	1.301	1.000
173	1.000	1000.000	1.411	1.000	2.321	1.000
174	3.301	2.648	2.870	4.460	1.310	6.222
176	1.000	2.341	3.042	3.134	1.000	3.053
177	2.156	1.405	2.065	1.000	1.193	1.000
179	1.765	1.000	1.759	1.000	1.181	1.000
180	2.129	6.089	3.899	1.000	2.196	1.000
181	3.204	2.833	4.328	4.755	1.000	3.492
182	1.000	1.000	1.783	1.000	1.309	2.859
183	1.000	0.622	3.478	1.000	1.000	2.075
184	1.000	1.000	1.546	1.000	1.377	1.000
185	1.000	1.000	1.546	1.000	1.377	1.000
190	3.265	1.667	1.616	3.653	1.000	4.325
191	3.265	1.667	1.616	3.653	1.000	4.325
192	3.556	2.703	2.625	5.822	1.992	5.800
193	3.612	2.805	2.581	5.251	2.012	5.542
194	21.643	4.895	7.904	1.000	14.168	1.000
198	3.064	1.638	1.653	1.000	1.000	4.661
200	2.522	1.665	2.326	1.000	1.452	3.272
201	3.655	1.518	2.510	1.000	2.121	1.000
202	4.129	2.770	2.591	5.639	3.005	3.796
204	2.580	1.610	1.898	4.129	1.785	3.871
205	2.580	1.610	1.898	4.129	1.785	3.871
206	2.814	1.671	2.417	2.969	1.933	2.916
207	2.334	2.605	3.906	3.916	2.139	3.279
208	3.139	2.202	2.073	1.000	1.151	2.845
209	2.217	1.951	2.949	1.000	1.340	4.517
209	1.000	1.000	1.000	1.000	1.366	1.000
210	4.359	1.000	2.725	1.000	2.553	6.608
211	4.402	2.294	1.447	3.511	1.481	6.705
212	0.335	3.413	4.285	4.598	3.878	0.623
213	4.317	2.395	2.300	1.000	2.783	6.710
214	1.000	1.000	1.363	1.000	1.260	1.000
215	1.563	1.000	2.704	1.000	3.385	1.000
217	1.000	1000.000	1.000	1.000	1.350	1.000
218	1.000	1.000	2.501	4.109	2.193	1.000
220	1.392	1.433	2.465	1.000	0.880	1.000
222	2.354	2.322	5.890	2.330	1.471	4.197

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
223	3.191	1.000	1.000	1000.000	1.190	1.000
224	2.194	2.716	4.944	2.383	4.697	3.205
225	3.301	3.965	4.760	4.521	2.457	3.939
226	3.908	1000.000	1.000	1.000	2.353	1.000
227	2.376	2.110	3.080	1.000	1.242	2.107
228	5.066	16.154	2.388	1000.000	1.845	1.000
230	1.513	2.197	37.637	1.000	2.547	1.000
231	2.269	1000.000	3.181	1.000	3.537	1.000
232	3.197	2.179	1.827	1.000	1.139	4.913
233	2.069	1.424	1.858	1.000	1.000	1.000
234	2.440	1.588	1.359	3.130	2.185	2.723
235	1.659	4.718	1.647	3.570	1.343	10.602
236	1.453	2.167	1.916	3.400	1.545	3.645
239	1.000	1000.000	1.000	1.742	1.254	5.545
240	2.085	1000.000	1.000	1.000	1.000	1000.000
242	1.000	1000.000	1.000	1.000	1.000	1.000
243	2.393	3.094	3.606	1.000	0.767	1.861
247	2.412	1.000	1.678	1.000	1.293	1.000
248	2.765	1.000	1.000	1.000	1.000	1.000
249	1.000	1.000	1.448	1.000	1.000	1.000
250	1.000	1000.000	1.679	1.000	1.000	1.000
252	4.550	5.133	2.834	1.000	1.000	5.286
253	2.151	1.000	1.000	1.000	1.000	1.000
254	1.915	2.126	1.834	1.000	1.442	4.586
255	1000.000	1.000	1000.000	1.000	1.000	1.000
256	1.850	1000.000	4.071	1.000	1.000	1.000
257	2.639	3.286	1.000	1.000	1.000	10.870
258	1.879	2.285	2.171	1.000	1.286	1.000
260	2.160	3.461	4.514	1.000	1.056	3.084
262	1.885	3.322	5.503	4.925	1.000	1.199
263	3.154	4.569	5.264	2.807	0.832	3.738
264	2.884	1.000	3.752	1.000	1.354	2.182
265	2.729	2.631	5.108	1.000	1.783	4.799
266	1.815	2.404	2.580	1.000	1.572	3.271
267	2.936	2.523	2.408	1.000	1.390	1.000
268	1.000	1000.000	3.221	1.000	1.000	1.000
269	1.157	12.605	11.085	1.000	0.672	16.116
270	1.907	2.012	2.563	1.000	1.395	2.964
271	3.349	2.129	4.127	5.991	1.397	3.621
272	1.000	1000.000	1.000	1.000	1.000	1.000

Table6
Microarray Data

SEQ ID NO	266Ratio	268Ratio	278Ratio	296Ratio	339Ratio	341Ratio
273	1.000	1000.000	3.181	1000.000	1.616	1.000
273	2.581	1000.000	3.053	1000.000	1.380	1.000
273	2.546	1.987	2.179	1000.000	1.521	
274	2.773	3.392	2.806	1.000	1.000	1.000
274	3.281	1000.000	2.659	1.000	1.000	5.308
274	2.265	2.564	2.594	4.592	1.261	
275	2.492	1000.000	2.809	1.000	1.362	1.000
275	2.563	1000.000	2.723	1.000	1.349	1.000
275	2.317	2.024	2.095	8.121	1.507	
276	11.393	6.491	9.734	1000.000	1.991	1.558
277	2.141	1000.000	2.898	1.000	1.681	1.000
277	2.144	1000.000	2.849	1.000	1.644	1.000
277	1.920	2.092	2.555	1.000	1.981	
278	1.000	1.000	1.000	1.000	1.479	1.000
278	1.000	1.000	1.000	1000.000	1.315	1.000
278	1.000	1.000	1.882	1000.000	1.000	
279	8.854	21.797	1.000	1.000	2.693	13.615
280	1.000	1.000	1.521	1000.000	2.118	1.000
280	1.000	1.000	1.639	1.000	1.000	1.000
280	1.941	2.016	1.344	1000.000	2.626	
281	1.635	3.641	2.622	6.280	0.828	3.262
282	2.845	1.830	1.000	1.579	1.421	3.361
283	1.987	1.823	2.217	3.073	1.000	1.946
284	1.000	0.339	1.154	1.000	0.683	7.198
285	2.563	2.748	4.634	2.607	1.866	4.879
286	2.548	1.744	3.466	1.000	1.310	3.598
287	2.250	2.202	2.421	1.000	1.263	3.736
288	2.646	4.745	0.001	1.000	1.611	6.078
289	1.277	2.238	1.546	1.398	0.740	1.629
290	2.386	4.979	1.000	1.000	1.368	2.528
293	1.682	4.449	4.047	1.000	1.890	3.255
294	2.627	1.980	1.809	5.603	1.130	6.009
295	2.072	3.446	1.629	5.465	1.395	5.743
296	2.453	3.789	3.013	1000.000	1.409	8.982
298	14.629	4.213	1.161	13.382	1.176	15.530
299	1.000	3.987	1.990	1.000	0.661	1.000
300	1.905	4.013	3.925	1000.000	1.000	1000.000
301	1.000	1.000	1.166	1000.000	1.239	1000.000
302	2.159	1.692	1.956	8.126	1.683	2.039
303	2.986	1.000	1.000	1.000	1.342	1.000
304	2.819	1.982	2.014	3.878	1.084	3.139
305	1.622	3.208	1.000	6.044	1.872	4.605
306	2.457	2.244	2.463	5.060	1.726	4.373
307	2.087	4.549	5.769	2.821	1.000	3.960
308	1.258	1.600	2.471	1.000	1.293	2.470
309	3.424	2.159	2.139	1.000	1.257	10.189

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
1	1000.000	1000.000	1.000	1.000	1.965	1000.000
2	1000.000	1.000	3.145	2.266	1.000	1000.000
2	1000.000	1.000	2.501	1.952	1.633	3.109
3	1000.000	1000.000	1.000	1.000	1.965	1000.000
4	1.000	1.000	1000.000	14.137	1.468	1.000
5	4.320	3.847	5.241	0.750	2.038	5.023
6	3.760	1.922	1000.000	0.614	3.491	3.299
7	4.200	1.597	1.000	2.709	8.594	2.212
9	1000.000	1.000	1.000	1.611	1000.000	1000.000
10	9.268	2.201	1.000	3.151	3.370	5.381
11	1.000	1000.000	1000.000	3.917	4.416	5.182
12	1.000	1.000	1000.000	3.667	1000.000	1.000
13	1000.000	1.000	1000.000	1.443	1.000	1000.000
14	4.419	1.464	1000.000	1.612	2.445	1.536
15	1000.000	1.000	1000.000	2.873	1000.000	1000.000
16	2.085	1.000	1000.000	3.990	1.000	1.700
17	9.599	6.384	1000.000	9.022	4.040	8.368
18	1000.000	2.624	1000.000	2.644	1000.000	1.000
19	7.669	1.585	1.536	1.575	1000.000	2.928
20	4.806	2.585	1.000	2.187	1.000	2.740
21	8.984	1.598	1.000	1.651	2.827	2.874
22	1.000	4.227	1000.000	12.460	1.000	0.723
23	1.000	1000.000	1000.000	1.000	1000.000	1000.000
24	4.717	1000.000	1000.000	1.354	1.999	2.046
25	4.164	1.794	1000.000	0.001	1000.000	1000.000
26	1.000	1.545	1000.000	2.682	2.395	1.000
27	2.575	1.000	1.000	1.466	1.559	1.781
28	0.801	1.000	1000.000	5.424	4.311	1.000
29	1.000	2.105	1.000	1.409	1000.000	1000.000
30	1000.000	1.000	1000.000	0.001	1.000	1.000
31	1000.000	1.932	2.654	1.000	1000.000	2.325
32	2.667	1.769	2.846	4.838	3.931	2.526
33	4.385	1.715	1.000	1.714	1.878	2.721
34	1.000	1.609	1000.000	1.000	1.714	1.897
35	1000.000	1.000	1.000	2.267	1.000	1000.000
36	2.631	1.000	1000.000	1.838	1.000	1.000
37	4.224	1.000	1.000	1.000	1.000	1000.000
38	6.252	1.273	1.000	0.786	2.448	3.145
39	1000.000	1.000	2.352	1.776	1.000	1000.000

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
40	2.120	1.600	1000.000	1.000	1.000	1.614
41	1000.000	1000.000	1000.000	1.000	1000.000	2.069
42	7.402	1.441	1000.000	1.497	1.000	4.146
43	4.691	2.357	1.643	1.817	1.869	3.243
44	3.258	1.000	1000.000	2.599	2.020	2.472
45	6.274	1000.000	1000.000	4.180	1000.000	1.925
46	4.621	1.523	1.000	1.569	1.239	2.517
47	2.081	1.000	1000.000	1.241	1.000	2.592
48	1.000	1.000	2.024	1.448	2.318	1.952
49	1.000	1.718	1.369	1.000	1.851	1.000
50	1.000	1.000	1000.000	1.544	1000.000	1.000
51	1000.000	1.000	1000.000	1.000	1.000	1.000
52	1.000	1000.000	1000.000	1.608	1.605	1.000
53	0.572	1000.000	1000.000	2.979	0.640	0.460
54	1.000	2.073	1.000	1.000	1.000	1.000
56	1000.000	1.000	1.000	1.000	1000.000	1000.000
57	1000.000	1.000	1000.000	3.338	1000.000	1000.000
58	1.000	1.563	1.859	1.671	3.492	2.044
59	4.498	5.094	9.629	23.761	4.153	3.452
60	1.000	1.469	1.328	1.669	1.522	1.504
61	4.052	1.833	1.000	1.143	2.077	1.000
62	12.427	4.425	1000.000	2.255	1.000	4.335
63	1.000	12.541	1000.000	32.178	1.000	3.556
64	1000.000	1.000	1000.000	1.000	1000.000	1.000
65	1.000	1.000	1000.000	1.000	1000.000	1.000
66	3.222	1.541	1000.000	2.620	1.000	1000.000
67	4.417	1.000	1000.000	1.000	4.157	1.000
68	1.000	1.397	1000.000	1.670	1.000	2.751
70	3.726	1.528	1000.000	1.000	2.523	1.987
71	5.196	1.872	0.819	0.671	1.000	2.942
73	1000.000	2.600	1.000	0.001	2.316	2.375
74	1000.000	3.243	2.513	2.051	3.513	5.099
75	1.000	1000.000	1.000	1.000	1.206	1000.000
76	1.000	2.055	1.768	0.400	1.000	3.026
77	1.000	2.454	1000.000	2.468	1000.000	1.000
78	5.495	1.554	1000.000	1.000	1.000	3.341
79	1000.000	1.000	1000.000	1.000	1000.000	1000.000
80	7.010	3.830	1000.000	7.324	4.914	9.844
81	3.172	1.000	1000.000	1.000	1.478	1.000
82	3.801	1.000	1.000	2.273	2.715	2.255

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
83	1.000	1.383	1000.000	1.467	1.000	1.581
84	4.002	1.580	1.697	1.194	2.134	2.081
85	1.000	2.692	2.070	2.061	3.125	4.431
86	6.560	2.001	2.497	1.249	2.839	3.138
87	1.000	1.365	1.000	1.511	1.000	3.133
88	1000.000	1.000	1.000	1.000	1.000	1.000
89	1000.000	3.661	1.986	3.888	2.374	1.505
90	1000.000	1.812	2.751	1.492	2.694	1000.000
91	1.883	1.416	2.024	4.332	2.187	1.645
92	6.213	1.655	1000.000	1.000	3.193	3.122
93	1.000	1.000	1.000	2.079	1.733	1.921
94	4.992	2.177	1.328	1.000	2.881	2.573
95	1000.000	1.000	1000.000	2.159	1000.000	1.000
96	1.000	2.086	2.476	2.037	2.493	1.932
97	2.587	1.582	3.324	1.577	2.375	1.912
98	1000.000	1000.000	4.172	10.317	7.421	1.000
99	1000.000	1.000	1.998	1.222	1.726	1.000
100	4.005	1.948	1.618	0.819	1.924	3.564
101	3.019	1.526	1.608	1.413	2.771	2.735
102	1000.000	1.000	1.000	2.091	1.423	1000.000
104	1000.000	2.432	2.000	2.886	1000.000	5.291
106	8.387	2.830	1.966	1.545	3.847	3.976
107	1000.000	1.000	1.000	0.767	1.424	1.000
108	1000.000	1.898	1.000	2.259	1.849	1.946
109	6.408	2.226	1.803	1.000	4.130	3.915
110	1000.000	1.000	1000.000	1.469	1.553	1.000
111	1000.000	1000.000	1000.000	0.001	1000.000	1.000
112	2.330	1.000	3.096	1.474	2.245	1.793
113	1.000	1.000	1000.000	4.494	2.593	4.069
114	4.286	1.800	1.236	2.192	1.650	2.265
116	1000.000	2.600	1.000	0.001	2.316	2.375
118	1000.000	1.000	3.145	2.266	1.000	1000.000
118	1000.000	1.000	2.501	1.952	1.633	3.109
119	1000.000	1.000	1000.000	2.244	1.000	1.000
120	6.047	2.225	2.982	1.979	3.446	4.035
121	1000.000	1.000	1.000	0.001	1000.000	1.000
122	1.000	1000.000	1000.000	1.000	1.901	1000.000
123	1000.000	5.082	12.392	10.761	13.505	1000.000
124	1000.000	5.082	12.392	10.761	13.505	1000.000
125	1000.000	4.256	1.000	1.000	2.584	1.000

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
126	1000.000	4.256	1.000	1.000	2.584	1.000
130	11.585	9.254	5.154	3.530	1.000	1000.000
131	1.000	1000.000	1.000	1.000	1.206	1000.000
132	4.992	2.177	1.328	1.000	2.881	2.573
133	4.992	2.177	1.328	1.000	2.881	2.573
134	1.000	1000.000	1.000	1.000	1.206	1000.000
135	1000.000	1000.000	1.000	0.001	1000.000	1.000
136	1.000	1.000	1.000	2.079	1.733	1.921
138	1000.000	1.000	3.145	2.266	1.000	1000.000
138	1000.000	1.000	2.501	1.952	1.633	3.109
140	1000.000	1.563	1.000	2.009	1.831	1000.000
141	1000.000	1000.000	4.239	5.417	1000.000	1.000
142	1.000	1.365	1.000	1.511	1.000	3.133
143	1.000	1.365	1.000	1.511	1.000	3.133
144	1000.000	1.812	2.751	1.492	2.694	1000.000
145	5.499	4.681	2.177	1.625	2.962	3.744
147	3.011	2.098	1.078	2.619	2.584	4.248
148	7.669	1.585	1.536	1.575	1000.000	2.928
149	1.744	1.429	1.252	6.226	1.641	0.502
150	1.869	1.625	0.759	2.887	1.000	2.315
151	1000.000	1.932	2.654	1.000	1000.000	2.325
152	6.865	1.835	4.215	1.727	4.036	3.607
152	1.000	1000.000	1.000	1.000	1000.000	1000.000
153	6.865	1.835	4.215	1.727	4.036	3.607
153	1.000	1000.000	1.000	1.000	1000.000	1000.000
154	4.971	1.791	1.844	1.365	3.329	2.184
155	4.672	1.313	2.916	1.821	1.336	3.305
156	1.000	1.472	1.223	1.400	1.505	2.037
157	1.648	1.000	1.582	1.358	1.727	1.760
159	4.620	3.118	7.531	6.538	4.646	1.000
161	1.328	1.464	1.833	1.528	1.000	1.568
162	1.000	1.000	11.454	1.000	1000.000	1.635
163	4.622	1.811	1.971	1.320	3.710	2.323
164	1.582	1.923	3.955	3.218	2.012	1.492
165	5.934	0.875	9.714	1.098	0.766	3.919
166	1.000	1.573	1.446	0.856	1.580	2.837
168	1.737	1.520	2.065	1.000	1.903	1.532
169	3.059	2.143	0.811	3.030	1.000	3.694
170	1.000	1.000	3.178	1.000	1.000	2.410
171	3.329	1.869	1.744	1.000	1.841	2.158

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
171	2.944	1.520	1.412	0.924	1.413	2.007
172	3.329	1.869	1.744	1.000	1.841	2.158
172	2.944	1.520	1.412	0.924	1.413	2.007
173	1000.000	1.000	1.000	0.001	1000.000	2.550
174	3.122	1.579	1.875	0.780	1.748	2.593
176	1.000	1.000	1.000	1.422	1.909	1.823
177	1.000	1.000	1000.000	0.001	1.175	2.484
179	2.109	1.000	3.422	1.398	1000.000	1.844
180	5.010	1.961	2.945	1.278	1.000	5.284
181	3.714	2.432	1.934	1.854	2.906	4.622
182	1.000	1.139	1.165	1.000	1000.000	3.798
183	2.098	2.058	3.397	2.165	1.182	1.826
184	1.000	3.270	2.451	5.451	1000.000	2.484
185	1.000	3.270	2.451	5.451	1000.000	2.484
190	4.259	2.220	0.849	0.818	1.877	3.175
191	4.259	2.220	0.849	0.818	1.877	3.175
192	4.909	3.162	1.000	1.000	4.064	2.673
193	4.530	3.045	1.000	1.000	3.838	2.576
194	1.000	6.905	21.410	34.505	4.944	5.930
198	3.867	2.189	0.857	0.816	1.997	3.042
200	4.166	2.261	1.181	1.109	2.298	2.709
201	2.355	1.425	1.550	1.131	2.126	3.107
202	3.464	2.557	2.610	3.169	2.748	2.796
204	3.068	2.490	1.725	1.000	3.184	2.938
205	3.068	2.490	1.725	1.000	3.184	2.938
206	3.489	2.059	1.254	0.625	2.074	4.658
207	3.845	1.487	2.039	1.177	1.945	4.156
208	1.000	1.309	1.625	1.000	1.844	3.536
209	3.356	1.807	2.006	1.193	1.649	2.452
209	1000.000	1.000	1000.000	1.000	1000.000	1000.000
210	4.998	1.924	3.786	1.626	2.532	3.055
211	4.539	2.618	0.813	1.000	2.077	1.816
212	4.841	1.329	4.911	2.083	2.357	3.937
213	5.131	2.395	1.814	0.835	1.948	2.510
214	1000.000	0.674	1000.000	1.000	1000.000	1.000
215	4.699	1.850	2.208	1.000	2.236	1.000
217	1000.000	1.000	1.000	1.000	1000.000	2.583
218	2.669	2.047	6.511	4.771	2.022	2.469
220	1.000	1.000	1000.000	1.000	1.000	2.304
222	1000.000	1.653	1.000	0.890	1.206	2.938

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
223	1000.000	2.245	1.000	1.566	2.445	1000.000
224	2.469	1.463	2.372	3.816	2.913	2.016
225	5.681	1.858	1.841	1.872	2.348	4.163
226	1000.000	1000.000	2.348	1.923	1.000	1.000
227	1000.000	1.670	1.353	2.361	1.694	1.677
228	11.585	9.254	5.154	3.530	1.000	1000.000
230	1.000	2.026	54.853	8.589	1.000	4.543
231	1000.000	2.006	1.000	1.645	1.850	2.971
232	6.106	2.211	1.000	0.655	2.426	2.896
233	1000.000	1.442	1.000	0.001	1.000	1.948
234	2.412	1.997	1.169	1.000	2.510	2.583
235	4.192	1.999	2.694	2.184	2.646	1.662
236	3.462	2.939	1.000	1.000	1.915	3.257
239	1.000	1.000	1000.000	1.404	1.968	2.770
240	1.000	1000.000	1000.000	1.240	1.000	1.000
242	1.000	1.000	1.000	1.000	1000.000	1000.000
243	1.000	1.886	1.579	1.000	1.879	2.810
247	4.205	1.767	1.173	0.894	1.000	2.442
248	1000.000	1.000	1000.000	0.001	1000.000	1000.000
249	1.000	1.000	2.232	1.000	1.000	1000.000
250	1.000	1.449	1.640	0.001	1000.000	2.069
252	3.817	1.922	4.059	4.718	1.000	1.000
253	1000.000	1.000	1.000	0.001	1000.000	1.000
254	1000.000	2.056	1.982	2.682	3.217	1.893
255	1000.000	1.000	1000.000	1.000	1.000	1.000
256	1000.000	1.000	1000.000	0.001	1000.000	1000.000
257	1000.000	1.000	1000.000	1.000	1.000	1000.000
258	1.000	1000.000	1000.000	1.000	1.839	1.358
260	1000.000	1000.000	2.263	1.694	3.345	4.212
262	3.413	1.735	2.477	1.457	1.972	2.175
263	3.244	1.694	8.613	1.388	3.850	1.919
264	4.713	2.122	1.634	2.056	2.147	1.786
265	6.991	2.807	2.647	2.373	2.771	2.691
266	3.874	2.295	0.712	1.388	2.355	2.762
267	7.346	1.685	1.614	1.000	3.996	3.786
268	1000.000	2.905	4.661	0.001	1000.000	6.672
269	1.526	1.000	31.528	24.386	0.759	1.000
270	5.080	2.319	0.574	1.222	1.538	2.368
271	6.032	2.507	1.653	1.431	4.391	2.676
272	1000.000	1.000	1000.000	0.001	1000.000	1.000

Table6
Microarray Data

SEQ ID NO	356Ratio	360Ratio	392Ratio	393Ratio	413Ratio	505Ratio
273	1.000	1.842	1000.000	0.001	1000.000	3.053
273	1000.000	1.818	1000.000	0.001	1000.000	3.055
273			2.043	0.690	5.216	2.997
274	4.227	2.603	2.261	1.171	1000.000	2.239
274	4.280	2.593	2.317	1.000	1000.000	2.120
274			2.150	1.283	4.145	2.697
275	1000.000	1.786	2.304	0.595	1000.000	3.015
275	1000.000	1.885	2.653	0.615	1000.000	2.987
275			1.803	0.548	3.949	3.435
276	11.331	5.503	15.840	6.935	3.358	8.487
277	4.324	2.114	2.842	1.000	1000.000	2.885
277	4.280	2.233	2.886	1.000	1000.000	2.995
277			2.464	1.000	5.011	3.606
278	1.000	1.000	1000.000	0.001	1000.000	1000.000
278	1.000	1.000	1000.000	0.001	1000.000	1000.000
278			1.674	1.000	1.000	2.051
279	1.000	1000.000	9.196	8.982	1.000	1.000
280	1000.000	1.501	1000.000	1.961	1000.000	1000.000
280	1.000	1.000	1000.000	2.189	1000.000	1000.000
280			1.000	2.598	1.000	2.240
281	4.879	2.044	0.699	1.260	2.833	2.065
282	1000.000	1000.000	1000.000	1.460	1000.000	1000.000
283	1.000	1.000	1000.000	1.182	2.676	2.017
284	1.000	2.755	0.751	0.525	0.372	2.141
285	1.000	1.338	2.277	2.063	3.160	2.606
286	4.868	2.141	1.334	1.275	3.223	2.607
287	3.200	1.804	1.000	1.540	1.620	3.287
288	1000.000	1.000	1.701	2.147	1000.000	1000.000
289	1.652	1.110	1.000	0.782	1.408	1.582
290	1.000	1.000	2.374	1.948	2.939	4.987
293	5.906	1.851	1.859	1.499	2.043	4.937
294	5.301	2.124	1.000	0.635	2.137	2.803
295	4.165	1.684	0.659	0.701	2.318	3.509
296	2.420	1000.000	1.000	1.403	1.000	2.887
298	8.587	5.084	5.104	0.697	2.896	6.393
299	1000.000	1000.000	1.880	1.000	1.589	0.673
300	1.000	1.000	2.701	1.982	1.000	2.927
301	1000.000	1000.000	1000.000	1.000	1.000	1.000
302	4.130	1.771	1.269	0.840	1.829	2.258
303	1000.000	1000.000	1000.000	1.000	1.000	1.000
304	4.246	2.205	1.000	1.000	2.004	2.989
305	5.515	2.000	1.212	0.571	3.954	3.995
306	3.655	1.733	2.095	1.287	2.583	2.649
307	3.009	1.826	6.895	1.539	3.720	2.069
308	1.897	1.511	1000.000	1.733	1.313	1.432
309	6.162	2.278	1.254	1.083	3.608	3.250

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
1	2.674	1.000	1.948	3.370	1000.000
2	2.349	4.031	4.241	3.734	1000.000
2	1.942	2.867	3.861	3.831	1000.000
3	2.674	1.000	1.948	3.370	1000.000
4	6.221	1.000	1.745	1.548	1000.000
5	1.000	0.595	2.318	3.850	1.000
6	1.353	1.788	2.232	2.879	1000.000
7	2.175	1.123	2.755	3.469	3.708
9	1.000	1.000	1000.000	1.000	1.000
10	2.577	2.417	6.630	1.221	1.000
11	1.000	1.000	1.610	4.134	1000.000
12	6.800	2.509	2.163	4.232	1000.000
13	1.000	1.229	1.000	6.374	1000.000
14	1.000	1.511	1.000	1.977	1000.000
15	1.000	1.686	1000.000	1.000	1000.000
16	1.387	1.000	1.000	1.633	1000.000
17	6.661	1.000	4.341	5.627	1000.000
18	1.000	1.381	3.083	5.510	1000.000
19	2.580	2.832	3.404	1.807	1000.000
20	1.814	1.738	1.000	2.211	1000.000
21	2.185	1.392	1.982	1.956	1000.000
22	1.957	0.363	3.166	5.641	1000.000
23	1.000	1.000	1.000	1.711	1000.000
24	1.999	1.379	1.588	1.526	1000.000
25	1.000	2.470	1000.000	3.090	1000.000
26	5.053	1.000	1.587	2.363	1000.000
27	1.740	1.000	1.325	1.211	4.442
28	0.606	0.845	1.000	2.007	1000.000
29	2.298	1.000	1000.000	1.000	1000.000
30	1.000	1.000	1.000	0.001	1.000
31	0.755	2.034	2.937	3.202	1000.000
32	4.147	0.617	2.755	2.027	1000.000
33	1.616	1.000	1.444	2.291	1.000
34	1.729	1.000	1.000	2.104	1.000
35	1.000	1.418	3.145	1.957	1000.000
36	0.902	1.551	1.330	1.531	1000.000
37	1.627	1.000	2.647	1.000	1.000
38	2.107	0.831	1.521	2.904	5.343
39	1.642	0.827	1.000	3.646	1000.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
40	2.131	1.000	1.635	1.283	1000.000
41	1.000	1000.000	1000.000	1.649	1000.000
42	2.264	1.509	2.556	2.220	1000.000
43	1.925	1.000	1.580	2.766	1000.000
44	1.499	0.632	1.639	3.285	1.000
45	2.662	4.012	3.615	2.484	1000.000
46	1.630	1.926	1.848	2.774	1000.000
47	1.733	2.061	2.422	2.974	1000.000
48	1.344	1.000	1.458	3.007	1000.000
49	2.752	0.685	2.848	4.770	1.000
50	1.000	1.000	1.000	1.860	1.000
51	1.000	1.000	1.000	4.959	1000.000
52	1.000	1.814	1.997	1.000	1000.000
53	1.000	0.573	1.000	1.000	1000.000
54	3.370	1.000	2.638	0.683	1.000
56	1.000	1.928	3.834	8.775	1000.000
57	2.254	0.273	1.000	16.397	1000.000
58	1.000	1.000	3.725	13.923	1000.000
59	7.443	0.781	4.559	1.891	1.953
60	1.366	1.637	2.433	2.570	1.794
61	1.000	1.207	1.868	3.020	1000.000
62	2.122	1.999	1000.000	7.584	1000.000
63	33.429	0.590	19.093	7.978	1.000
64	1.000	1.000	1.000	0.001	1.000
65	1.000	1.100	1000.000	3.258	1000.000
66	1.552	2.333	1.657	3.515	1000.000
67	1.989	1.935	1.000	2.694	1000.000
68	2.572	1.879	2.355	2.697	1000.000
70	1.943	1.331	2.036	1.853	1000.000
71	0.623	1.609	1.819	2.230	1000.000
73	1.000	1.000	2.368	4.462	1.000
74	2.250	2.511	4.406	6.237	1000.000
75	1.000	1.993	1.000	3.367	1.000
76	1.954	2.892	5.009	10.929	1.000
77	1.000	2.208	1.000	3.700	1000.000
78	2.545	1.512	1.711	2.197	1000.000
79	1.000	1000.000	1000.000	1.636	1000.000
80	8.786	1.000	3.801	4.470	1000.000
81	1.224	1.000	1.840	2.479	1000.000
82	2.134	1.725	1.574	1.690	1.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
83	1.814	1.000	1.247	1.836	1000.000
84	1.147	1.480	2.247	2.355	1000.000
85	1.757	1.794	4.007	4.360	1000.000
86	3.047	1.890	2.847	2.003	1000.000
87	1.000	1.000	2.196	6.107	1.000
88	1000.000	3.924	2.074	1.913	1.000
89	2.311	4.970	4.016	2.705	1000.000
90	3.475	2.143	2.722	1.934	1000.000
91	1.000	1.000	1.661	3.722	1.000
92	3.827	1.748	2.305	1.981	1000.000
93	1.000	2.184	2.190	2.887	1000.000
94	1.505	1.866	2.201	2.311	1.000
95	1.000	1.000	1.000	0.001	1000.000
96	2.875	1.853	3.641	3.234	1000.000
97	1.890	1.409	2.753	2.896	1.000
98	1.000	1.000	1.840	1.415	1000.000
99	2.240	2.147	2.480	2.211	1.000
100	2.313	1.000	1.898	3.687	1000.000
101	1.420	4.866	1.721	2.785	1000.000
102	1.000	1.562	1.214	1.313	1.000
104	0.786	1.000	4.372	4.805	1000.000
106	1.805	2.612	3.803	2.195	1000.000
107	1.530	2.497	1.554	3.618	1000.000
108	1.770	1.763	2.889	2.312	1000.000
109	1.877	5.748	5.708	4.087	1000.000
110	1.000	1.000	2.239	0.001	1000.000
111	1.000	1000.000	1.786	1.000	1000.000
112	1.726	1.485	2.394	3.030	13.359
113	1.698	1.798	4.950	2.034	1000.000
114	1.085	2.082	2.442	2.553	9.085
116	1.000	1.000	2.368	4.462	1.000
118	2.349	4.031	4.241	3.734	1000.000
118	1.942	2.867	3.861	3.831	1000.000
119	1.822	1.000	5.179	3.767	1000.000
120	2.037	1.643	4.383	5.198	1000.000
121	1.000	1.000	1.000	1.000	1000.000
122	1.000	12.667	1.000	0.001	1000.000
123	2.575	4.044	13.979	9.017	1000.000
124	2.575	4.044	13.979	9.017	1000.000
125	2.466	4.966	4.521	20.801	1000.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
126	2.466	4.966	4.521	20.801	1000.000
130	4.880	6.177	4.566	14.060	1000.000
131	1.000	1.993	1.000	3.367	1.000
132	1.505	1.866	2.201	2.311	1.000
133	1.505	1.866	2.201	2.311	1.000
134	1.000	1.993	1.000	3.367	1.000
135	1.000	1.000	4.652	7.125	1000.000
136	1.000	2.184	2.190	2.887	1000.000
138	2.349	4.031	4.241	3.734	1000.000
138	1.942	2.867	3.861	3.831	1000.000
140	2.006	3.757	2.910	2.197	1000.000
141	1.000	1000.000	1.000	1.794	1000.000
142	1.000	1.000	2.196	6.107	1.000
143	1.000	1.000	2.196	6.107	1.000
144	3.475	2.143	2.722	1.934	1000.000
145	1.000	4.216	2.640	5.844	1000.000
147	1.530	1.572	1.827	2.313	1000.000
148	2.580	2.832	3.404	1.807	1000.000
149	0.281	1.000	3.764	1.529	1.220
150	1.518	2.075	1.790	2.765	1.000
151	0.755	2.034	2.937	3.202	1000.000
152	2.147	4.153	3.398	6.222	1000.000
152	1000.000	1000.000	1.000	1.000	1.000
153	2.147	4.153	3.398	6.222	1000.000
153	1000.000	1000.000	1.000	1.000	1.000
154	1.627	2.357	2.874	1.981	4.449
155	2.463	1.533	2.386	1.712	1.000
156	1.408	1.470	2.145	2.281	1000.000
157	1.198	1.521	2.450	2.453	1.000
159	2.671	1.000	6.475	2.887	1.000
161	0.634	1.000	1.887	2.954	1.000
162	3.689	1.284	6.136	10.074	1000.000
163	1.568	2.604	3.259	2.098	8.596
164	7.291	1.000	2.272	1.269	1.000
165	11.479	0.711	0.455	1.669	1000.000
166	2.643	1.116	1.437	2.002	1000.000
168	1.419	2.482	2.422	1.772	1000.000
169	1.870	1.777	2.835	3.218	1000.000
170	1.316	1.000	1.600	1.646	3.057
171	1.684	1.000	1.711	1.000	1.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
171	1.563	1.000	1.395	2.611	1000.000
172	1.684	1.000	1.711	1.000	1.000
172	1.563	1.000	1.395	2.611	1000.000
173	1.000	1.000	2.845	2.271	1000.000
174	2.348	2.323	3.503	5.909	1.000
176	2.347	1.697	1.786	1.774	1000.000
177	1.217	1.770	2.235	1.000	1000.000
179	1.246	3.009	2.349	3.329	1.000
180	2.179	1.541	3.515	3.526	1.000
181	2.048	1.839	3.305	5.198	1000.000
182	1.000	1.705	1.614	2.713	1000.000
183	2.385	1.000	1.548	2.007	1.665
184	1.836	1.000	6.206	2.436	1.000
185	1.836	1.000	6.206	2.436	1.000
190	1.133	2.208	2.880	2.389	9.982
191	1.133	2.208	2.880	2.389	9.982
192	3.414	3.666	4.715	2.491	16.521
193	3.284	3.491	4.456	2.425	1000.000
194	13.171	0.733	6.575	2.731	1000.000
198	1.127	2.233	2.880	2.433	9.032
200	1.703	2.222	2.974	2.894	7.449
201	4.377	2.084	2.910	1.502	2.442
202	2.470	1.000	2.979	2.180	3.352
204	1.730	2.613	3.395	2.582	6.789
205	1.730	2.613	3.395	2.582	6.789
206	1.825	2.529	2.791	1.963	4.459
207	1.944	1.907	3.119	2.585	3.617
208	1.439	2.501	3.414	2.843	1000.000
209	3.770	1.603	2.493	2.925	1.000
209	1.314	1.728	1.263	1.197	1000.000
210	2.267	3.522	2.655	5.232	1.000
211	1.000	2.615	2.618	2.503	11.726
212	7.843	0.041	1.878	0.217	1000.000
213	3.899	10.877	6.454	3.144	1.956
214	1.246	1.000	1.000	1.181	1000.000
215	3.172	3.222	2.475	2.160	1.000
217	1.000	1.000	1.523	2.609	1000.000
218	3.293	1.000	1.000	2.732	2.192
220	1.000	1.287	2.129	3.522	1000.000
222	1.176	1.972	2.334	2.913	1000.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
223	1.474	2.581	4.499	3.593	1000.000
224	3.662	2.629	2.538	4.035	1000.000
225	2.853	1.621	2.144	4.622	1.000
226	3.271	2.265	1.459	1.918	1000.000
227	2.137	2.033	1.671	2.244	1.000
228	4.880	6.177	4.566	14.060	1000.000
230	3.074	26.948	45.948	1.657	1000.000
231	1.745	2.245	3.446	2.189	1000.000
232	1.522	2.008	1.905	2.135	1000.000
233	1.301	1.644	1.608	2.573	1000.000
234	0.892	1.320	3.327	2.251	6.064
235	2.470	3.131	2.893	5.198	15.764
236	1.310	1.767	3.355	2.085	9.093
239	1.000	1.000	3.494	2.109	1.000
240	1.000	1.000	2.892	0.001	1.000
242	1.000	1.000	1.000	0.001	1.000
243	1.393	1.386	2.483	2.914	1000.000
247	1.257	1.265	2.119	1.611	1.638
248	1.310	1000.000	1.000	2.645	1000.000
249	0.721	1.000	3.990	3.979	1000.000
250	1.000	1.778	2.139	2.523	1.000
252	2.436	1.000	2.391	3.722	1.000
253	1.000	1.000	1.000	0.001	1000.000
254	1.000	1.125	4.459	2.566	4.438
255	1.000	1.000	1.000	1.000	1000.000
256	2.137	0.860	1.917	1.927	1000.000
257	1.000	1.224	3.925	6.743	1.000
258	1.000	1.937	2.634	2.772	1.000
260	3.084	2.107	3.455	2.720	1.000
262	1.532	1.351	1.666	1.000	1.000
263	2.915	1.000	3.686	4.443	5.787
264	2.801	1.000	2.800	1.317	21.941
265	1.317	1.399	3.968	4.372	1000.000
266	1.109	1.768	2.102	2.776	1.000
267	1.769	2.193	3.417	2.684	1000.000
268	1.110	1.350	3.099	5.162	1000.000
269	1.000	1.106	1.000	1.247	1000.000
270	1.359	1.759	1.717	2.348	1.000
271	1.875	1.976	3.761	3.589	1.000
272	1.000	0.404	1.000	2.699	1000.000

Table6
Microarray Data

SEQ ID NO	517Ratio	534Ratio	546Ratio	577Ratio	695Ratio
273	1.818	1.343	2.128	2.268	1000.000
273	1.893	1.431	2.114	2.418	1000.000
273	1.414	1.000	1.830	2.189	
274	1.327	1.737	3.002	2.128	1000.000
274	1.364	1.918	2.488	2.051	1000.000
274	1.000	1.000	2.592	1.989	
275	1.922	1.482	1.000	2.398	1000.000
275	1.883	1.542	1.000	2.373	1000.000
275	1.490	1.000	1.961	2.280	
276	6.882	1.000	3.803	7.214	1000.000
277	1.585	1.740	2.986	2.547	1000.000
277	1.575	1.690	3.075	2.510	1000.000
277	1.000	1.000	2.194	2.478	
278	2.044	1.447	1.894	1.958	1000.000
278	1.801	1.560	1.988	1.000	1000.000
278	1.000	1.000	1.000	2.368	
279	9.032	7.176	1000.000	2.163	1.000
280	1.000	1.304	5.493	3.650	1000.000
280	1.000	1.000	1000.000	3.790	1000.000
280	1.000	0.891	1000.000	4.766	
281	1.850	2.122	1.902	3.735	10.769
282	1.000	1.515	1.000	3.660	1.000
283	1.853	1.000	2.451	2.219	1.000
284	3.100	0.688	0.343	0.949	2.324
285	1.862	2.133	2.516	2.968	3.792
286	1.802	1.885	3.121	3.004	1000.000
287	1.737	1.925	1.567	1.783	1000.000
288	1.000	1.464	2.544	0.001	1000.000
289	1.000	1.000	1.556	2.268	2.007
290	1.571	1.000	4.774	4.348	1.000
293	2.404	1.627	2.663	2.434	7.687
294	1.493	2.623	2.342	2.262	10.295
295	1.501	2.268	1.769	2.146	10.584
296	2.278	6.035	1.563	3.268	1.000
298	1.000	0.609	2.361	4.332	1000.000
299	2.021	1.000	1.186	1.108	1000.000
300	1.000	1.494	3.425	4.016	1000.000
301	1.000	0.501	2.938	4.948	1000.000
302	1.372	1.000	2.737	2.096	9.209
303	1.373	2.545	1.740	1.964	1000.000
304	1.248	1.511	3.172	2.846	13.323
305	1.579	2.065	2.615	2.177	12.724
306	1.381	1.947	3.714	2.110	13.446
307	3.014	1.197	3.800	4.375	5.410
308	1.550	1.681	2.045	1.800	2.389
309	1.260	1.861	3.293	2.906	21.009

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
1	1.632	2.733	1.000	1.089	2.298
2	2.888	1000.000	1000.000	1.000	1.748
2	2.437	2.765	3.823	1.754	2.818
3	1.632	2.733	1.000	1.089	2.298
4	1.348	1.000	3.062	3.667	1.000
5	1.605	1.000	4.493	1.195	0.492
6	1.598	1.755	2.254	2.234	4.357
7	1.000	1000.000	3.953	2.069	4.353
9	3.538	1000.000	1000.000	0.882	1000.000
10	3.236	1.000	1.644	3.907	3.309
11	1.748	3.040	4.812	1.265	4.644
12	1000.000	1000.000	1.000	3.451	1000.000
13	1.000	2.429	1.000	1.000	1.390
14	1.966	1000.000	2.366	1.273	2.604
15	1.000	1.000	1.000	2.900	1000.000
16	1.000	1.000	65.380	3.911	1.000
17	1.000	1000.000	8.733	2.372	1000.000
18	1000.000	1.000	1.000	0.471	1000.000
19	1.121	1.928	2.007	3.021	1.000
20	1.000	1000.000	1.000	1.000	1.000
21	1.000	1.539	1.873	1.390	2.992
22	1000.000	1000.000	1.000	8.984	1000.000
23	1.000	1.000	54.274	1.000	1000.000
24	1.000	1.000	1.783	1.368	1.000
25	1.000	1.000	3.335	1.886	1000.000
26	1.000	1000.000	80.443	1.887	1.000
27	1.932	1.484	1.819	1.000	1.737
28	1.000	1.000	1.000	1.994	1.000
29	1.000	1.000	1.000	0.674	1000.000
30	1.396	1.619	1000.000	1.000	1000.000
31	2.330	1.605	1.000	1.371	1.861
32	15.314	1.000	2.483	1.301	2.530
33	1.000	1000.000	3.985	1.000	2.647
34	1.000	1000.000	1.858	1.000	1.801
35	1.000	2.100	1.000	1.000	0.567
36	1.743	0.772	1.778	0.916	1.000
37	1.000	1000.000	1.000	0.620	1000.000
38	1.472	1.576	2.243	1.519	2.006
39	1.791	2.111	1.000	1.476	0.770

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
40	1.000	1000.000	1.000	1.581	1.000
41	1000.000	1.000	1.000	1.000	1000.000
42	1.739	1.000	3.510	1.813	3.313
43	1.547	2.011	2.143	1.355	1.648
44	0.717	2.643	5.245	1.986	5.832
45	2.603	3.166	1.691	2.000	2.178
46	2.574	1.000	2.288	1.392	1.230
47	2.788	1.000	3.423	1.410	1.000
48	1.753	2.178	1.000	1.000	1.000
49	1.000	2.110	2.922	1.221	1.818
50	0.629	2.199	1.000	1.000	0.323
51	1.000	4.200	1.000	1.000	1.568
52	1.709	1.952	2.138	1.997	2.592
53	4.009	8.967	3.131	1.000	1.000
54	1.000	1.752	1.000	1.000	0.329
56	1.260	3.598	1.000	1.000	3.663
57	1000.000	3.414	0.457	1.000	1.000
58	1.000	1.283	3.577	0.424	1.298
59	2.422	9.461	2.426	15.888	5.998
60	2.101	1.718	3.691	1.267	2.438
61	2.229	1.283	3.356	1.000	1000.000
62	2.571	1000.000	5.048	2.216	5.440
63	5.099	1000.000	3.086	4.829	1000.000
64	1.000	7.750	1.000	2.622	1000.000
65	2.267	1000.000	1.000	0.339	1.000
66	2.927	1000.000	2.090	1.711	1.000
67	1.000	1000.000	2.294	1.000	1000.000
68	1.000	1000.000	1.931	1.603	1.639
70	1.454	1.000	2.236	1.868	1.000
71	1.582	1000.000	2.159	1.154	3.133
73	1.830	2.012	1.000	1.000	4.490
74	4.092	2.717	5.829	2.364	6.823
75	3.420	2.017	1.000	1.000	1.000
76	0.477	2.033	6.476	1.000	8.716
77	15.842	5.611	2.577	3.145	2.296
78	2.748	2.326	2.039	1.000	1.000
79	1.000	1.000	1.000	1.000	1000.000
80	1.000	7.267	9.652	2.032	5.416
81	1.000	1000.000	1.863	1.000	1000.000
82	1.000	3.170	2.426	1.679	3.508

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
83	1.000	1.000	2.392	2.446	2.417
84	1.000	1.000	2.149	2.426	2.233
85	1.000	2.549	2.585	1.931	5.929
86	1.222	2.723	2.159	2.238	4.179
87	1.000	1.000	1.000	2.055	1.000
88	2.011	2.388	1.000	1.421	3.370
89	3.397	3.121	1.886	2.332	5.285
90	1.496	2.040	4.899	3.374	4.268
91	1.770	2.304	2.212	1.517	1.000
92	1.000	3.701	3.181	2.761	4.151
93	0.833	2.292	2.302	2.888	3.397
94	1.000	1.000	2.035	3.513	4.309
95	1.000	1.000	1.000	1.000	0.506
96	1.715	4.531	2.769	2.295	2.282
97	1.902	1.947	2.574	1.248	2.805
98	4.781	1000.000	5.006	27.177	2.613
99	1.707	1.905	1000.000	2.054	2.497
100	2.225	2.040	2.376	1.000	5.228
101	2.161	1.000	1.000	2.030	5.134
102	1.000	1.000	1.000	1.622	2.248
104	1.463	2.259	1000.000	0.695	1.000
106	1.379	2.755	2.181	5.752	4.575
107	1.000	1.000	1.000	2.191	2.526
108	2.225	2.542	1.000	2.510	2.757
109	1.000	2.285	2.732	3.860	1.000
110	1.000	2.154	1.569	0.830	1.694
111	1000.000	1.000	1.000	1000.000	1000.000
112	2.008	1.981	2.817	1.212	3.158
113	7.255	2.745	6.156	1.000	3.627
114	1.000	2.396	2.817	2.137	2.414
116	1.830	2.012	1.000	1.000	4.490
118	2.888	1000.000	1000.000	1.000	1.748
118	2.437	2.765	3.823	1.754	2.818
119	1.849	3.024	1000.000	1.524	2.251
120	2.108	2.183	3.102	2.288	2.250
121	5.843	1.000	1000.000	1.000	0.631
122	1.000	7.525	1.000	1.000	6.152
123	19.279	7.008	4.519	2.931	1.000
124	19.279	7.008	4.519	2.931	1.000
125	11.073	4.042	1000.000	2.758	3.710

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
126	11.073	4.042	1000.000	2.758	3.710
130	0.589	2.190	1.000	14.048	7.702
131	3.420	2.017	1.000	1.000	1.000
132	1.000	1.000	2.035	3.513	4.309
133	1.000	1.000	2.035	3.513	4.309
134	3.420	2.017	1.000	1.000	1.000
135	2.171	1000.000	1.000	1.000	1000.000
136	0.833	2.292	2.302	2.888	3.397
138	2.888	1000.000	1000.000	1.000	1.748
138	2.437	2.765	3.823	1.754	2.818
140	1.000	3.533	1.000	1.564	1.000
141	1.000	1000.000	1000.000	2.130	1.000
142	1.000	1.000	1.000	2.055	1.000
143	1.000	1.000	1.000	2.055	1.000
144	1.496	2.040	4.899	3.374	4.268
145	8.122	1.840	1000.000	2.076	4.246
147	1.532	1.784	1.788	2.692	3.889
148	1.121	1.928	2.007	3.021	1.000
149	0.733	1.620	1.185	3.314	2.749
150	1.252	1.641	3.038	1.645	2.293
151	2.330	1.605	1.000	1.371	1.861
152	3.962	3.367	4.967	1.000	4.753
152	1.489	1000.000	1.000	1000.000	1000.000
153	3.962	3.367	4.967	1.000	4.753
153	1.489	1000.000	1.000	1000.000	1000.000
154	1.000	2.366	2.968	3.289	3.888
155	1.000	2.101	2.128	1.382	5.451
156	1.555	1.850	2.158	1.554	2.206
157	1.687	1.391	2.044	1.794	1.000
159	1.775	2.939	8.436	8.001	4.705
161	1.685	1.000	2.039	1.568	1.809
162	1.000	1.000	1.000	4.823	1000.000
163	1.000	2.436	3.673	3.739	4.114
164	1.310	1.177	2.153	3.484	2.882
165	0.816	1.000	1.533	0.510	5.978
166	6.314	1.925	2.834	1.465	5.021
168	1.250	1.415	1.000	3.106	1.912
169	1.277	3.240	3.356	1.330	4.338
170	1.322	1.139	2.449	1.000	3.947
171	1.477	1.514	3.023	1.910	2.604

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
171	1.375	1.000	3.144	1.633	2.118
172	1.477	1.514	3.023	1.910	2.604
172	1.375	1.000	3.144	1.633	2.118
173	1.355	1.667	1000.000	3.185	1.000
174	1.946	2.190	5.343	2.681	2.893
176	1.395	1.000	2.720	1.911	1.000
177	1.287	2.187	1000.000	1.955	1000.000
179	1.942	1.648	3.371	1.846	2.356
180	1.172	3.415	2.121	4.349	4.004
181	2.415	2.364	6.401	2.234	2.905
182	1.000	1.934	4.498	1.000	1000.000
183	1.829	1.000	1.716	1.423	1.000
184	0.775	1.000	1000.000	1.000	1.667
185	0.775	1.000	1000.000	1.000	1.667
190	0.732	1.000	2.740	2.007	1.718
191	0.732	1.000	2.740	2.007	1.718
192	1.000	2.927	3.737	4.809	4.353
193	1.000	5.023	3.859	4.839	4.306
194	3.215	1.000	1000.000	50.989	15.479
198	0.700	1.000	2.707	1.979	1.884
200	1.000	1.935	2.245	3.344	2.720
201	1.112	3.845	3.389	3.337	3.843
202	1.304	4.280	2.632	7.486	3.088
204	0.958	1.800	2.566	2.848	2.167
205	0.958	1.800	2.566	2.848	2.167
206	1.000	2.207	1.643	3.429	3.091
207	1.236	1.905	2.114	2.845	1.000
208	1.430	2.275	1000.000	2.000	1.000
209	1.844	2.214	3.090	1.604	1.497
209	1.260	1.000	1.000	2.322	1000.000
210	3.970	1.719	4.092	1.000	3.255
211	1.433	1.670	2.569	2.879	2.305
212	0.182	3.130	5.340	4.148	11.729
213	1.000	2.756	2.520	5.262	2.103
214	0.860	1.124	1000.000	1000.000	1000.000
215	0.875	1.368	1000.000	1000.000	1.000
217	1.368	1.000	1.000	1.351	1.000
218	1.877	1.657	7.367	2.116	3.058
220	1.000	0.848	1.000	1.159	1000.000
222	3.181	1.686	1000.000	1.000	1.917

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
223	2.019	3.737	1000.000	2.132	3.007
224	3.015	2.462	1000.000	2.879	2.239
225	2.610	3.036	3.688	4.161	6.185
226	1.000	2.937	1.000	1.000	1.000
227	3.131	3.982	1.862	1.000	2.417
228	0.589	2.190	1.000	14.048	7.702
230	1.964	1.503	6.416	7.304	1.000
231	1.000	2.165	1000.000	4.741	1.841
232	1.000	1.000	1.843	2.763	2.001
233	0.853	1.992	1000.000	1.728	2.257
234	1.000	1.000	2.334	2.930	1.641
235	0.572	1.000	5.377	4.294	4.499
236	1.000	1.000	2.031	2.597	2.624
239	1.286	2.041	1.000	1.000	0.831
240	1.792	1.432	1.000	1.000	1.000
242	1000.000	1.000	1.000	1.000	0.172
243	1.928	1000.000	1000.000	1.710	1.000
247	1.000	2.083	1.000	1.710	1.970
248	1.301	1.291	1000.000	1000.000	1000.000
249	1.740	1.293	1000.000	2.082	1.000
250	1.975	1000.000	1000.000	1000.000	1000.000
252	4.999	2.937	4.307	2.202	3.590
253	1000.000	1.871	1000.000	1.000	1.000
254	1.158	1.000	2.822	1.820	2.095
255	1.000	1.455	1000.000	1.000	1.000
256	1.938	2.420	1.000	1.000	1.000
257	1.000	2.948	3.313	0.717	5.690
258	1.517	2.159	1.000	1.000	1.707
260	1.161	2.231	2.036	1.000	2.520
262	1.472	1.980	2.421	2.123	4.204
263	1.506	1.000	4.130	1.666	7.534
264	1.838	2.096	3.816	1.583	3.523
265	2.165	2.152	1000.000	2.174	3.436
266	1.000	4.230	3.708	2.680	2.847
267	1.232	2.387	2.242	3.180	1.953
268	1.613	1.000	1000.000	1.000	1000.000
269	1.000	1.000	1.000	1.365	1.000
270	1.000	4.243	3.378	2.227	3.604
271	1.000	2.753	2.836	2.694	3.157
272	1.000	1.000	2.477	0.401	1.000

Table6
Microarray Data

SEQ ID NO	784Ratio	786Ratio	791Ratio	888Ratio	889Ratio
273	1.000	2.114	1.000	1000.000	1000.000
273	1.000	2.093	1000.000	1000.000	1000.000
273	1.000	1000.000	1.913	2.293	1.000
274	1.176	2.003	3.872	5.122	1.000
274	1.133	1.872	3.810	4.563	2.212
274	1.000	1.000	3.274	3.889	1.779
275	1.000	2.372	1.893	1000.000	1000.000
275	1.000	2.236	1.000	2.298	1.000
275	1.000	1.000	1.956	1.864	1.000
276	1.000	8.051	10.173	2.841	3.924
277	1.000	2.046	2.397	1000.000	3.266
277	0.903	2.037	2.463	3.430	3.127
277	1.000	1.000	1000.000	1000.000	1000.000
278	1.000	2.197	1.000	1.000	1.000
278	1.000	2.176	1.000	1.000	1.000
278	1.558	1.000	1000.000	1.000	1.000
279	1.600	7.052	4.524	5.885	13.545
280	0.890	3.520	1000.000	1000.000	1000.000
280	0.894	1.000	1000.000	1000.000	1000.000
280	1.000	1000.000	1.000	1.189	1000.000
281	1.000	1.000	8.802	1.000	3.801
282	2.249	1.484	1.000	1.000	1.428
283	1.268	1.506	1.858	1.289	1.570
284	2.057	8.399	1.000	1.000	2.366
285	1.000	1.877	3.090	1.530	3.361
286	1.000	2.125	2.399	2.598	2.175
287	2.822	1.837	2.258	1.172	1.848
288	2.480	3.808	1.000	2.335	1.000
289	1.886	1.000	2.036	1.000	2.274
290	1.836	2.924	2.495	1.000	3.389
293	1.000	1.000	2.551	1.791	3.236
294	1.000	1.000	1.889	2.541	1.944
295	1.000	1.000	3.395	2.218	1.660
296	2.189	2.797	3.920	2.084	5.442
298	1.613	2.289	7.737	1.433	1.262
299	1.819	1.999	2.052	1.620	0.708
300	1.683	2.334	1.000	1.000	0.735
301	1.645	2.684	1000.000	1.303	1.000
302	1.000	2.040	1.931	2.613	1.720
303	7.206	2.272	1.000	1.550	0.611
304	1.395	1.550	3.044	3.929	1.882
305	1.000	1.000	2.339	2.113	2.510
306	1.000	1.000	2.061	3.040	2.786
307	2.070	1.705	4.074	1.446	3.838
308	1.999	1.534	2.167	1.597	2.850
309	1.314	1.439	3.176	4.294	2.141

Table 7
Antisense Knock-out ("KO") Results

SEQ ID NO	CID	GeneAssignment	GeneSymbol	GenBank Gene Name	mRNA KO
4	1	Homo sapiens S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4) mRNA > :: gb|M80563|HUMCAPL Human CAPL protein mRNA, complete cds.	S100A	S100A4	>80%
9	6	CDC28 protein kinase 2	CKS2	CKS2 01/ 11	>80%
11	8	Fn14 for type I transmenmbrane protein	LOC51330	Fn14	>90%
12	9	cadherin 3, P-cadherin (placental)	CDH3	CADHERIN-P	>90%
16	13	kallikrein 6 (neurosin, zyme)	KLK6	proteaseM	>80%
17	14	arachidonate 5-lipoxygenase	ALOX5	ALOX5	>80%
22	18	bone morphogenetic protein 4	BMP4	BMP4	>90%
25	21			GSTHOM	>90%
32	27	cathepsin H	CTSH	CATH-H	>90%
38	33	transketolase (Wernicke-Korsakoff syndrome)	TKT	TRANSKETOLASE	>90%
41	36	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)	FUT1	FUT1	>90%
42	37	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	PCBD	hDohc	>95%
54	50			THC271862	>70%
56	53			hECT2	>80%
63	63	dipeptidase 1 (renal)	DPEP1	DPP	>80%
71	74	ClpP (caseinolytic protease, ATP-dependent, proteolytic subunit, E. coli) homolog	CLPP	CLPP	>80%
77	75	tetraspan 5	TSPAN-5	NET-4	>90%
78	76	phosphoserine aminotransferase	PSA	serAT	>90%
87	121	EGF-like-domain, multiple 2	EGFL2	EGFL2	>70%
100	127	sigma receptor (SR31747 binding protein 1)	SR-BP1	SR-BP1	>90%
113	92	tumor protein D52-like 1	TPD52L1	hD53	>80%
141	143	sulfotransferase family 2B, member 1	SULT2B1	SULT2B1	>80%
147	166	over-expressed breast tumor protein	OBTP	HUMTUM	>90%
165	179	amphiregulin (schwannoma-derived growth factor)	AREG	AREG	>90%
180	193	S-adenosylhomocysteine hydrolase	AHCY	HUMAHCY2	>70%
183	196	hypothetical protein [Homo sapiens]	HSPC152	c719	>80%
208	155	glyoxalase I	GLO1	GLO1	>90%
213	160			c374641	>80%
214	161	putative nucleotide binding protein, estradiol-induced [Homo sapiens]	E2IG3	c454001	>80%
218	164	interferon induced transmembrane protein 2 (1-8D)	IFITM2	1-8U	>90%
233	263	polo (Drosophia)-like kinase	PLK	PLK1	>90%
236	266	serum-inducible kinase	SNK	SNK	>80%
239	269	sterile-alpha motif and leucine zipper containing kinase AZK [Homo sapiens]	ZAK	AZK	>70%
242	273			AA399596	>70%
253	280	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	AKT3	>90%
276	227			ITAK1	>90%
279	239			AI335279	>90%
285	242	serine hydroxymethyltransferase 2 (mitochondrial)	SHMT2	SHMT2	>90%
294	245	serum/glucocorticoid regulated kinase-like	SGKL	SGKL	>90%
295	248	mitogen-activated protein kinase kinase 4	MAP2K4	MKK4	>80%
300	249	TTK protein kinase	TTK	hTTK	>90%
123, 124	103	stearoyl-CoA desaturase	SCD	SCD	>90%
130, 228	115	prostate differentiation factor	PLAB	PLAB	>80%
162, 193	176	kallikrein 10	KLK10	NES1	>80%
182, 217	195			c1665	>80%

Table 7
Antisense Knock-out ("KO") Results

SEQ ID NO	CID	GeneAssignment	GeneSymbol	GenBank Gene Name	mRNA KO
247, 290	236	serine/threonine kinase 15	STK15	hARK2	>80%
257, 268	212	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CDKN3	KAP	>85%
31, 151	170	pituitary tumor-transforming 1	PTTG1	PTTG1	>90%
35, 150	30	CDC28 protein kinase 1	CKS1	CKS1	>80%
5, 298, 301	2	EphB3 [Homo sapiens]	EPHB3	EPHB3	>90%
65, 220	65	KIAA0101 gene product [Homo sapiens]	KIAA0101	KIAA0101	>80%
73, 116	100	KIAA0175 gene product [Homo sapiens]	KIAA0175	KIAA0175	>90%
75, 131, 134	106	catenin (cadherin-associated protein), alpha-like 1	CTNNAL1	RTA00000179AF.k.22.1	>90%
8, 106	5	AXL receptor tyrosine kinase	AXL		>95%
88, 196	118			c3376	>80%

Table 8
Functional Assay Data

SEQ ID NO	CID	GeneAssignment	Gene Symbol	Gene	mRNA KO	Proliferation	Softagar
4	1	Homo sapiens S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4) mRNA > :: gb|M80563|HUMCAPL Human CAPL protein mRNA, complete cds.	S100A	S100A4	>80%	Inhib in SW620	weak inhibition
11	8	Fn14 for type I transmenmbrane protein	LOC51330	Fn14	>90%	inconsis. SW620, 231	inhibits SW620, 231
12	9	cadherin 3, P-cadherin (placental)	CDH3	CADHERIN-P	>90%	Inhib in SW620	Inhib in SW620
16	13	kallikrein 6 (neurosin, zyme)	KLK6	proteaseM	>80%	weak effect in SW620	negative SW620
38	33	transketolase (Wernicke-Korsakoff syndrome)	TKT	TRANSKETOLASE	>90%	inconsis. SW620, 231	inhibits SW620, 231
42	37	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	PCBD	hDohc	>95%	inconsis. SW620, 231	inhibits SW620, 231
56	53			hECT2	>80%	Inhib in SW620	Inhib in SW620
63	63	dipeptidase 1 (renal)	DPEP1	DPP	>80%	weak inhibition	negative in SW620
77	75	tetraspan 5	TSPAN-5	NET-4	>90%	Inhib in SW620	weak inhibition
180	193	S-adenosylhomocysteine hydrolase	AHCY	HUMAHCY2	>70%	Inhib in SW620	Inhib in SW620
233	263	polo (Drosophia)-like kinase	PLK	PLK1	>90%	Inhib in SW620	Inhib in SW620
236	266	serum-inducible kinase	SNK	SNK	>80%	Inhib in SW620	negative in SW620
253	280	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	AKT3	>90%	inhibits SKOV3,231	inhibits SKOV3,231
279	239			AI335279	>90%	negative in SW620	weak inhibition
300	249	TTK protein kinase	TTK	hTTK	>90%	inhibits SW620	inhibits SW620
247, 290	236	serine/threonine kinase 15	STK15	hARK2	>80%	Inhib in SW620	weak effect in SW620
257, 268	212	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	CDKN3	KAP	>85%	Inhib in SW620	
35, 150	30	CDC28 protein kinase 1	CKS1	CKS1	>80%	Inhib in SW620	Inhib in SW620
88, 196	118			c3376	>80%	weak effect in SW620	neg SW620